

Two distinct trophectoderm lineage stem cells from human pluripotent stem cells

Adam Mischler¹, Victoria Karakis¹, Jessica Mahinthakumar¹, Celeste K. Carberry², Adriana San Miguel¹, Julia E. Rager², Rebecca C. Fry², Balaji M. Rao^{1,3*}

¹Department of Chemical and Biomolecular Engineering, North Carolina State University, Raleigh, North Carolina 27695, USA

²Department of Environmental Sciences and Engineering, Institute for Environmental Health Solutions, University of North Carolina - Chapel Hill, Chapel Hill, North Carolina 27599, USA

³Golden LEAF Biomanufacturing Training and Education Center (BTEC), North Carolina State University, Raleigh, North Carolina 27695, USA

*Corresponding author: Email: bmrao@ncsu.edu

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Running title

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Abstract

The trophectoderm layer of the blastocyst-stage embryo is the precursor for all trophoblast cells in the placenta. Human trophoblast stem (TS) cells have emerged as an attractive tool for studies on early trophoblast development. However, the use of TS cell models is constrained by the limited genetic diversity of existing TS cell lines, and restrictions on using human fetal tissue or embryos needed to generate additional lines. Here we report the derivation of two distinct stem cell types of the trophectoderm lineage from human pluripotent stem cells. Analogous to villous cytotrophoblasts *in vivo*, the first is a CDX2⁻ stem cell comparable to placenta-derived TS cells – they both exhibit identical expression of key markers, are maintained in culture and differentiate under similar conditions, and share high transcriptome similarity. The second is a CDX2⁺ stem cell with distinct cell culture requirements, and differences in gene expression and differentiation, relative to CDX2⁻ stem cells. Derivation of TS cells from pluripotent stem cells will significantly enable construction of *in vitro* models for normal and pathological placental development.

Introduction

Specification of the trophectoderm and the inner cell mass is the first differentiation event during human embryonic development. The trophectoderm mediates blastocyst implantation in the uterus and is the precursor to all trophoblast cells in the placenta. Upon embryo implantation, the trophectoderm forms the cytotrophoblast (CTB), a putative stem cell that can differentiate to form the two major cell types in the placenta – the extravillous trophoblast (EVT) and the syncytiotrophoblast (STB) (1, 2). The EVTs are involved in remodeling of uterine arteries, which is critical to ensure adequate perfusion of the placenta with maternal blood, whereas the multinucleated STB mediates the nutrient and gas exchange at the maternal-fetal interface (3, 4). Abnormalities in trophoblast development are associated with pregnancy-related pathologies such as

miscarriage, preeclampsia and placenta accreta. Yet, despite its relevance to maternal and fetal health, constraints on research with human embryos and early fetal tissue impede mechanistic insight into early trophoblast development.

Trophoblast stem (TS) cells derived from first trimester human placental samples and blastocyst-stage embryos have emerged as an attractive *in vitro* model system for early human trophoblast (5). However, restricted accessibility of embryos and placental samples from early gestation and low genetic diversity of existing cell lines limit the use of this model. In contrast, human pluripotent stem cells (hPSCs) are a more accessible source for generating *in vitro* models of human trophoblast. More importantly, unlike early gestation primary samples where the projected pregnancy outcome is uncertain, human induced pluripotent stem cells (hiPSCs) can potentially provide models of validated normal and pathological trophoblast development (6). However, whether *bona fide* trophoblast can be obtained from hPSCs has been a subject of intense debate (7). A rigorous head-to-head comparison between trophoblast derived from hPSCs and their *in vivo* counterparts has proven difficult due to multiple reasons. Previous studies have used varying experimental protocols (8), both primary placental samples and cultures of terminally differentiated trophoblast obtained from hPSCs exhibit heterogeneity and contain many cell types, and until recently self-renewing TS-like cells had not been derived from hPSCs (9–12).

In this study, we report the derivation and maintenance of two distinct trophectoderm lineage stem cell types from hPSCs, specifically human embryonic stem cells (hESCs) and hiPSCs, in chemically defined culture conditions. The first is a CDX2⁻ stem cell that is comparable to TS cells derived from early gestation placental samples and similar to the villous CTB. The second is a CDX2⁺ cell type with distinct cell culture requirements, and differences in gene expression and differentiation, relative to CDX2⁻

stem cells. Critically, the isolation of self-renewing stem cell populations allowed a direct comparison of placenta-derived TS cells with TS cells from hPSCs; genome wide transcriptomic analysis and functional differentiation assays demonstrate very high similarity between placenta- and hPSC-derived CDX2⁺ TS cells. The routine derivation of TS cells from hPSCs will provide powerful tools for mechanistic studies on normal and pathological early trophoblast development.

Results

A chemically defined medium containing S1P enables differentiation of hESCs to CTB.

Media formulations in previous studies on trophoblast differentiation of hESCs included components such as knockout serum replacement (KSR) or bovine serum albumin (BSA) that act as carriers for lipids. Albumin-associated lipids have been implicated in activation of G-protein coupled receptor (GPCR)-mediated signaling (13, 14). For instance, the phospholipid sphingosine-1 phosphate (S1P) present in KSR can activate YAP signaling. YAP plays a critical role in specification of the trophoblast in mouse (15–17), as well as human trophoblast development (18, 19). We investigated the use of S1P in the context of trophoblast differentiation of hESCs under chemically defined culture conditions, by modifying our previous protocol that utilized KSR (20, 21). H1 and H9 hESCs cultured in E8 medium were differentiated for 6 days in E7 medium (E8 without transforming growth factor-beta1 (TGFβ1)) supplemented with S1P, by treatment with BMP4 and the activin/nodal inhibitor SB431542 (**Figure 1A**). Under these conditions, we observed upregulation of the trophoblast marker *CDX2* and the CTB marker *ELF5* (**Figure S1A, B**). Upregulation of *TBX4* was observed after 6 days. However, overall there were no significant changes in markers associated with neural or mesodermal differentiation after 6 days suggesting that differentiation to these lineages did not occur (**Figure S1A, B**). Immunofluorescence analysis at day 6 confirmed

expression of the pan-trophoblast marker KRT7, and CTB markers P63 and GATA3; expression of *CDX2* was not observed (**Figure 1B**; **Figure S1C**).

The putative CTB cells obtained at day 6 were investigated for their ability to differentiate to EVT and STB, using protocols similar to those previously employed (20). We observed formation of mesenchymal cells from epithelial cells over a 6-day period when passaged into E8 medium supplemented with epidermal growth factor (EGF) and SB431542. Immunofluorescence analysis showed expression of KRT7 and the EVT markers VE-Cadherin and HLA-G (**Figure 1C, S1D**). Alternatively, passaging CTB-like cells in E6 medium (E8 without TGFβ1 and fibroblast growth factor-2 (FGF2)) supplemented with activin and EGF resulted in formation of KRT7⁺ multinucleate cells expressing the STB markers hCG and syncytin over an 8-day period (**Figure 1D, S1E**). Removal of S1P from the medium during hESC differentiation to CTB-like cells abolished formation of EVTs that express HLA-G and VE-Cadherin (**Figure 1E, S2A**) under identical differentiation conditions (**Figure 1A**). Differentiation to STB also did not occur in the absence of S1P, as evidenced by lack of expression of syncytin and KRT7 (**Figure 1F, S2B**). Also, downregulation of the trophoblast marker *CDX2* and upregulation of transcripts of neural and mesoderm markers was observed in cells after 6 days of differentiation, upon removal of S1P (**Figure S2C**). Taken together these results show that CTB-like cells – similar to those in previous studies utilizing more complex culture conditions (20) – can be obtained by differentiation of hESCs in a chemically defined medium containing S1P. Further, addition of exogenous S1P is necessary for hESC differentiation to trophoblast in our chemically defined culture medium.

Rho GTPase signaling, downstream of GPCRs activated by S1P, has been implicated in nuclear localization of YAP (22, 23). Both Rho/RhoA associated kinase (ROCK) and nuclear YAP play a critical role in trophoblast specification in the mouse (24, 25). Therefore, we investigated the role

of Rho/ROCK signaling and YAP in trophoblast differentiation of hESCs. The Rho/ROCK inhibitor Y-27632 was included during differentiation of hESCs to CTB-like cells and subsequent differentiation to EVT and STB to investigate the role of Rho/ROCK signaling. Under these conditions, HLA-G expression was observed in cells obtained from H9 hESCs; however, VE-Cadherin expression was weak and observed in only a few cells (**Figure S3A**). On the other hand, expression of EVT markers was not observed in cells derived from H1 hESCs. Additionally, presence of ROCK inhibition abolished STB formation, as shown by lack of expression of syncytin and KRT7 (**Figure S3B**).

To investigate the role of YAP signaling in CTB formation from hESCs, we used an hESC cell line (H9) that expresses an inducible shRNA against YAP (H9-YAP-ishRNA) or a scrambled shRNA control (26). YAP knockdown abolished differentiation to EVT and STB, as evidenced by lack of expression of the relevant markers. Notably, high cell death was observed (**Figure S3A, B**). Gene expression analysis revealed significant reduction in *ELF5* upon YAP knockdown, relative to the scrambled shRNA control (**Figure S3C**). Significant downregulation of the mesodermal genes *TBX4* and *LMO2* was observed, whereas *T* was upregulated, in H9-YAP-ishRNA, relative to the scrambled control. Taken together, these results show that Rho/ROCK signaling, and YAP are necessary for differentiation of hESCs to functional CTB that can give rise to both EVTs and STB, in our chemically defined culture medium.

S1P mediates its effects on trophoblast differentiation of hESCs through its receptors.

S1P acts through both receptor-mediated and receptor-independent pathways (14, 27). To investigate the specific mechanism of S1P action during hESC differentiation to trophoblast, we replaced S1P with D-erythro-dihydrospingosine-1-phosphate (dhS1P) in our protocol. dhS1P acts as an agonist for the S1P receptors (S1PRs) but

does not mediate an intracellular effect (28). Replacing S1P with dhS1P yielded similar results – CTB-like cells showed expression of CDX2, GATA3, P63, and TEAD4 (**Figure 2A; Figure S4A**). Upon further differentiation as previously described (**Figure 1A**), STB expressing KRT7 and hCG, and EVT expressing HLA-G and VE-Cadherin were obtained (**Figure 2B, C; Figure S4B, C**). These results suggest that S1PR signaling mediates the effect of exogenous S1P during hESC differentiation to trophoblast in our chemically defined medium.

S1P acts extracellularly through S1PR1-5 (14, 27), however TBs have been shown to only express S1PR1-3 (29). We further used selective chemical agonists for S1PR1-3 – CYM5442 hydrochloride, CYM5520 and CYM5541, respectively – to replace S1P in differentiation protocols previously discussed. Expression of CDX2, GATA3, P63, and TEAD4 was observed in CTB-like cells for all three agonists (**Figure 2A; Figure S4A**). Similarly, use of each agonist resulted in expression of the EVT markers HLA-G and VE-Cadherin, and formation of multinucleate STB expressing KRT7 and hCG (**Figure 2B, C; Figure S4B, C**). However, we observed some variability between the agonists (**Figure S5**). For instance, use of the S1PR2 agonist resulted in strong cytoplasmic expression of P63, and high heterogeneity in staining at day 6 relative to the other agonists. Formation of large multinucleated STB was more pronounced when the S1PR2 or S1PR3 agonists were used, as compared to the S1PR1 agonist. On the other hand, the S1PR1 and S1PR3 agonists enhanced formation of mesenchymal EVTs, relative to the S1PR2 agonist. Taken together, our results further confirmed that S1PR signaling mediates effects of exogenous S1P during trophoblast differentiation of hESCs in our culture system. Since our qualitative observations showed that use of the S1PR3 agonist resulted in expression of CTB markers, and both multinucleate STB and mesenchymal EVTs could be obtained when the S1PR3 agonist was used, we chose the S1PR3 agonist for subsequent studies.

Optimizing timing of hESC differentiation enables derivation of CDX2⁺ TS cells.

We investigated whether CTB-like cells obtained by treatment of hESCs with BMP4 and SB431542 in E7 medium supplemented with the S1PR3 agonist CYM5541 for 6 days could be passaged and maintained under conditions used for culture of blastocyst- and placenta-derived primary TS cells (5). Upon plating in trophoblast stem cell medium (TSCM) developed by Okae et al. (5), hESC-derived CTB-like cells underwent differentiation, and epithelial colonies could not be retained after a single passage. CDX2 expression is upregulated significantly in as little as 2 days after initiation of hESC differentiation, but decreases by day 6 (**Figure S1A, B**). Additionally, previous studies have reported differentiation of hESCs to CDX2⁺/p63⁺ cells upon treatment with BMP for 4 days (30). Therefore, we explored the use of a shorter differentiation step for obtaining CTB-like cells (**Figure 3A**). After 3 days of differentiation, H9 and H1 hESCs expressed nuclear CDX2, P63, and TEAD4 uniformly (**Figure 3B**). However, by day 6 most differentiated H1 and H9 hESCs lose expression of CDX2 (**Figure 3C**). Quantitative image analysis showed that nearly all cells are CDX2⁺ at day 3, in contrast to CTB-like cells at day 6. Notably, use of a 6-day protocol resulted in significantly reduced fraction CDX2⁺ cells in the case of H1 hESCs in comparison to the 3-day protocol; on the other hand, a significant fraction of H9 cells retained CDX2⁺ at day 6 (**Figure 3D**). Transcriptome analysis using RNA sequencing identified 291 genes with significantly higher expression levels, and 330 genes with significantly lower expression levels, in day 3 differentiated hESCs vs. undifferentiated hESCs (**Tables S1 and S2**). In addition to *CDX2*, expression of other trophoblast-associated markers such as *HAND1*, *GATA3*, and *TFAP2A* was upregulated in differentiated hESCs at day 3, whereas expression of pluripotency-associated *NANOG* was downregulated. Gene set enrichment analysis of differentially expressed genes identified 567 and 202 gene ontology (GO) cate-

gories (out of 9996 queried categories) associated with higher and lower gene expression in day 3 differentiated cells vs. undifferentiated hESCs, respectively (**Tables S3 and S4**). Consistent with differentiation to epithelial trophoblast, genes associated with the GO terms for epithelium development, epithelial cell proliferation, and epithelial cell differentiation were upregulated in day 3 differentiated hESCs.

CDX2⁺ cells at day 3 were passaged into a chemically defined medium containing four major components (denoted TM4) – the S1PR3 agonist CYM5541, the GSK3 β inhibitor CHIR99021, the TGF β inhibitor A83-01, and FGF10. CHIR99021 and A83-01 are components of TSCM used for culture of primary TS cells; FGF10 was included because FGFR2b signaling is active in blastocyst- and placenta-derived TS cells and the early placenta (5). Cells in TM4 could be maintained as epithelial colonies for 30+ passages over the course of 5 months. In TM4 medium, cells derived from H9 and H1 hESCs retained expression of the trophoblast markers CDX2, TFAP2C, YAP, TEAD4, and GATA3 (**Figure 3E; Figure S6**) (15, 17, 31–34). Additionally, cells expressed the pan-trophoblast marker KRT7, and low levels of P63. Notably, CDX2 expression has been strongly associated with the trophoblast and is lost once placental villi are formed (30, 35–37). To indicate that these cells are derived from hPSCs, and to distinguish these cells from TS cells that do not express CDX2, these cells are denoted as hPSC-TS^{CDX2} cells.

We further evaluated the differentiation potential of hPSC-TS^{CDX2} cells using same protocols as those used by Okae et al. for differentiation of primary TS cells to EVTs and STB (5). Cells were able to form multinucleate STB that expressed hCG and KRT7 (**Figure 3F**). However, upon EVT treatment, cells did not form mesenchymal elongated cells but acquired a flattened morphology. Upon passage, cells showed no HLA-G and minimal VE-Cadherin expression (**Figure 3G**). Further, cells maintained an epithelial flattened morphology with KRT7 expression, but sparse hCG expression.

CDX2/P63⁺ TS cells derived from hESCs can be maintained in medium used for primary TS cells.

We evaluated whether hPSC-TS^{CDX2} cells could be maintained in TSCM used for culturing primary TS cells (**Figure 3A**) (5). When hPSC-TS^{CDX2} cells cultured in TM4 for 5+ passages were directly passaged into TSCM, cells underwent a change in colony morphology over ~3 passages; however, very little differentiation was observed. Notably, cell morphology of the hESC-derived cells closely resembled that of placenta-derived TS cells in TSCM that was used as a control (**Figure S7**) (5). Strikingly, hPSC-TS^{CDX2} cells lost expression of CDX2 and gained higher expression of P63 in TSCM. As discussed earlier, cells could be maintained as epithelial colonies when hESCs after 3 days of differentiation were passaged into TM4. In contrast, passaging day-3 differentiated hESCs into TSCM resulted in extensive differentiation, although a few epithelial colonies could be observed. Further passaging resulted in similar morphological changes in the epithelial colonies as those observed for hPSC-TS^{CDX2} cells transitioning to TSCM. After ~ 6 passages, only epithelial colonies remained, and they closely resembled both the hPSC-TS^{CDX2} cells transitioned into TSCM and placenta-derived TS cells. H9 and H1 hPSC-TS^{CDX2} cells – passaged directly into TSCM after 3 days of differentiation or transitioned from TM4 (**Figure 3A**) – showed high expression of YAP, TEAD4, TFAP2C, and GATA3, similar to cells in TM4, but no expression of CDX2 (**Figure 4A; Figure S8A**). Further, they expressed the pan-CTB marker KRT7 (**Figure 4A, B; Figure S8A, B**). The hESC-derived cells cultured in TSCM exhibit similar expression profile of trophoblast markers as placenta-derived TS cells (**Figure S7A, B**). Therefore, these cells are denoted as hPSC-TS cells to indicate that they are derived from hPSCs.

We further evaluated the differentiation potential of hPSC-TS cells using the same protocols as those used by (5) for differentiation of primary TS cells to EVT and STB (5). Similar to placenta-derived TS cell controls (**Figure S7C-E**), hPSC-TS cells

could be differentiated into mesenchymal EVTs expressing HLA-G and VE-Cadherin (**Figure 4C,D; Figure S8C,D**), and multinucleate STB expressing hCG and KRT7 (**Figure 4F; Figure S8E**). Additionally, expression profile of transcripts corresponding to CTB, STB, and EVT markers upon differentiation of hPSC-TS cells was similar to those seen in case of placenta-derived TS cell controls (**Figure 4E,G**). Further, hPSC-TS cells have been maintained in TSCM for over 30 passages; they retain their ability to differentiate into STB- and EVTs after long-term culture in TSCM. Taken together along with differences in culture conditions for maintenance, differentiation behavior, and expression of the trophoderm marker CDX2, these results suggest that hPSC-TS^{CDX2} and hPSC-TS cells represent two distinct stem cell populations.

Transcriptome analysis confirms high similarity between hPSC-TS cells and placenta-derived TS cells and reveals differences between hPSC-TS^{CDX2} and hPSC-TS cells

We conducted genome wide transcriptome analysis on hPSC-TS^{CDX2}, hPSC-TS and placenta-derived TS (control) cells using RNA sequencing. Note that since hPSC-TS and placenta-derived TS cells are cultured under identical conditions, our analysis represents a direct comparison between transcriptome profiles across these two cell types. Principal component analysis (PCA) of transcriptomic signatures showed that hESC-derived and primary TS cells cluster together, indicating similarities in overall gene expression (**Figure 5A**). A Spearman Rank correlation test correlating average expression levels per gene between hPSC-TS and placenta-derived TS cells (**Figure 5B**), and hierarchical clustering analysis (**Figure 5C**), showed very high transcriptome similarity between hPSC-TS and placenta-derived TS cells. Note that 110 genes exhibit significant differential expression in hPSC-TS cells relative to placenta-derived TS cells (**Table S5**). In comparison, 109 genes show significant differentiation expression in hPSC-TS cells derived from H1 vs. H9

hESCs (**Table S6**), underscoring the high transcriptome similarity between hPSC-TS and placenta-derived TS cells. Thus, in conjunction with similarities in marker expression and culture conditions for maintenance and differentiation, these results confirm that hPSC-TS are analogous to placenta-derived TS cells.

PCA also showed that hPSC-TS^{CDX2} cells are a distinct cell type that cluster differently from hPSC-TS cells and hESCs differentiated to the trophoblast lineage for 3 days (**Figure 5A**). Statistical analysis of gene expression profiles identified genes that were significantly differentially expressed between hPSC-TS^{CDX2} and hPSC-TS. Specifically, 269 genes showed significantly higher expression levels, and 275 genes showed significantly lower expression levels in hPSC-TS^{CDX2} vs. hPSC-TS cells (**Tables S7 and S8**). Gene set enrichment analysis of these genes identified 300 and 47 gene ontology (GO) categories (out of 9996 queried categories) associated with genes showing higher and lower expression in hPSC-TS^{CDX2} vs hPSC-TS, respectively (**Tables S9 and S10**). Interestingly, consistent with differences in colony morphology between hPSC-TS^{CDX2} and hPSC-TS cells, genes associated with extracellular matrix, biological adhesion, and cell-cell adhesion were upregulated in hPSC-TS^{CDX2} cells. Taken together along with distinct medium requirements for maintenance in cell culture, and differences in EVT differentiation under identical assay conditions, these results show that hPSC-TS and hPSC-TS^{CDX2} represent distinct stem cell populations.

Higher expression of the trophoblast-associated markers *CDX2* and *HAND1* is observed in hPSC-TS^{CDX2} cells relative to hPSC-TS cells that are analogous to placenta-derived TS cells. On the other hand, expression of *TP63* – associated with villous CTB – is higher in hPSC-TS relative to hPSC-TS^{CDX2} (**Figure 5D**). To investigate the similarities between the human trophoblast and hPSC-TS^{CDX2} cells, we compared the transcriptome profiles of hPSC-TS^{CDX2}, hPSC-TS, and placenta-derived TS cells with the transcriptome of trophoblast cells

from human embryos (38). The Spearman Rank correlation test was used to correlate gene expression levels between primary trophoblast cells and hPSC-TS^{CDX2}, hPSC-TS, or placenta-derived TS cells (**Table S11**). The correlation R-values were similar for all three TS cell types, and lower than those generating when comparing between hPSC-TS cells and placenta-derived TS cells or hPSC-TS^{CDX2} and hPSC-TS cells. The lower correlation R-values are likely due to the differences between cells in culture and primary human embryos and experimental protocols for transcriptome analysis; trophoblast cells from human embryos were analyzed using single cell RNA sequencing, as opposed to bulk RNA sequencing in our study. Additional studies are necessary to investigate whether hPSC-TS^{CDX2} cells are analogous to cells of the human trophoblast.

hPSC-TS^{CDX2} and hPSC-TS cells can be generated from hiPSCs.

Lastly, we investigated if our results on derivation of hPSC-TS^{CDX2} and hPSC-TS cells from hESCs could be extended to hiPSCs. Accordingly, we used our previously described protocols (**Figure 3A**) to derive hPSC-TS^{CDX2} and hPSC-TS cells from the hiPSC line SC102A-1. hPSC-TS^{CDX2} cells derived from SC102A-1 hiPSCs maintained expression of *CDX2*, *TFAP2C*, *GATA3*, *YAP*, *KRT7*, and *TEAD4*, along with low expression level of *P63* in TM4 medium (**Figure 6A**). Similarly, hPSC-TS cells derived from SC102A-1 hiPSCs expressed *KRT7*, *P63*, *TEAD4*, *TFAP2C*, *YAP*, and *GATA3* in TSCM (**Figure 6B, C**). SC102A-1 hPSC-TS cells lost expression of *CDX2* but gained higher expression levels of *P63* and *KRT7* in TSCM. The proliferation rate of SC102A-1 hPSC-TS cells was also similar to that of placenta-derived TS cells (**Figure 6D**). Differentiation of hPSC-TS cells derived from SC102A-1 hiPSCs using protocols described by Okae et al. (5), resulted in formation of mesenchymal EVTs with high expression of *HLA-G* and *VE-Cadherin* (**Figure 6E, G**), and multinucleate STB expressing hCG and

KRT7 (**Figure 6I**). Expression profile of transcripts corresponding to CTB, STB, and EVT markers upon differentiation of SC102A-1 hPSC-TS cells was also similar to those seen in case of placenta-derived TS cell controls (**Figure 6F,H**). These results confirm that two distinct TS cell populations can also be derived from hiPSCs.

Discussion

In this study, we have shown that two distinct stem cell populations of the trophoctoderm lineage – hPSC-TS and hPSC-TS^{CDX2} – can be derived from hESCs and hiPSCs under chemically defined culture conditions. Whether *bona fide* trophoblast can be obtained from hPSCs has been a subject of debate (7). Despite extensive research in this area, conducting a rigorous head-to-head comparison between hPSC-derived and primary trophoblasts has been challenging. The isolation of trophoblast stem cell populations from hPSCs in this study, in conjunction with the recent derivation of primary TS cells from blastocysts and early gestation placental samples (5) enables such a comparison. We have shown that hPSCs can be differentiated to TS cells that express markers consistent with primary (placenta-derived) TS cells (P63, TEAD4, TFAP2C, YAP, and GATA3). The hPSC-derived hPSC-TS cells are cultured in the same medium as primary TS cells. They differentiate to EVT and STB using similar protocols as those used for primary TS cells. Further, hPSC-derived hPSC-TS and primary TS have highly similar transcriptomes. Taken together, these results show that hPSC-derived TS cells are analogous to primary TS cells, and that hPSCs can indeed differentiate to *bona fide* trophoblasts. In the time since our results were reported in preprint form (39), our approach for generation of TS cells from hPSCs has been independently confirmed; Shahbazi et al. used our protocol to generate hPSC-TS cells from hESCs overexpressing an E-Cadherin-GFP fusion (40). Our results are also consistent with other recent work that has demonstrated derivation of TS cells from hPSCs, although using different differentiation protocols and in

the absence of BMP treatment (11). In these studies, hiPSCs were differentiated to trophoblast cysts in micromesh cultures for 30-50 days, and subsequently TS cells were obtained by culturing cells from cysts in TSCM.

Comparison with other studies: role of specific culture conditions.

Previous studies on trophoblast differentiation of hESCs have employed differing protocols, resulting in significantly different outcomes in some cases. Bernardo et al. reported that BMP treatment of hESCs results in differentiation of hESCs to mesoderm and not trophoblast (41). More recently, multiple studies have investigated the differentiation of hPSCs to the trophoctoderm lineage. Dong et al. and Cinkornpumin et al. report the derivation of TS cells from naïve hPSCs, but not primed hPSCs (9, 10). In these studies, primed hPSCs did not give rise to TS cell lines when plated in TSCM that is used for maintenance of blastocyst- and placenta-derived TS cells in culture. Guo et al. claim that primed hPSCs do not undergo differentiation to the trophoctoderm lineage using a previously described protocol involving treatment with BMP; rather they suggest that primed hPSCs differentiate to cells of the amnion (42). However, the differentiation protocols used in these studies differs significantly from that used in this study for deriving hPSC-TS cells from hPSCs. Specifically, our results show that receptor-mediated signaling by the albumin-associated sphingolipid S1P plays a critical role in hESC differentiation to trophoblast in our medium. Notably, receptor-mediated S1P signaling has been implicated in blastocyst formation in mouse (43). Differences in results reported by previous studies may be due to variability in the lipid composition of media used during trophoblast differentiation of hESCs.

Another possible explanation for discrepancies in previous studies is that differences in media used for routine maintenance of undifferentiated hPSCs may contribute to differences in differentiation potential. For instance, unlike hESCs cultured in the presence of KSR, hESCs in E8 medium exhibit some features of naïve pluripotency (44).

Finally, further investigation is required to compare rigorously placenta-derived TS cells and cells of the human amniotic epithelium. It is important to note that we observe very high transcriptome similarity between hPSC-TS and placenta-derived TS cells (**Fig. 5A-C**), and conversion of primed hPSCs to TS cells using our approach has been independently replicated (40).

Differences between hPSC-TS^{CDX2} and hPSC-TS cells

Marker expression analysis, functional differentiation assays, and genome-wide transcriptome analysis confirm the high similarity between hPSC-TS and placenta-derived TS cells that are similar to villous CTB. However, hPSC-TS^{CDX2} cells differ significantly from hPSC-TS cells. They do not undergo differentiation to EVTs under the culture conditions used for differentiating hPSC-TS and primary TS cells. Moreover, transcriptome analysis shows that genes associated with several key pathways and biological processes are differentially regulated between hPSC-TS^{CDX2} and hPSC-TS cells. These results suggest that hPSC-TS^{CDX2} and hPSC-TS cells represent two distinct stem cell populations.

Significantly, hPSC-TS^{CDX2} cells – but not hPSC-TS – express high levels of the trophoderm-associated markers *CDX2* and *HAND1*, associated with putative trophoderm stem cells as proposed by (37). Further, hPSC-TS^{CDX2} cells can be readily transitioned into TSCM used for culturing hPSC-TS, as was seen by Okae et al. (5) when transitioning trophoderm cells of blastocysts into TSCM. Subsequently, hPSC-TS^{CDX2} lose expression of *CDX2* and express higher levels of *P63* in TSCM, and can differentiate to form EVTs and STB. Note that TS cells derived from the trophoderm in the blastocyst stage embryo lose expression of *CDX2* (5). On the other hand, it has not been possible yet to revert hPSC-TS to hPSC-TS^{CDX2} by culturing in TM4 medium. Finally, the trophoderm forms a primitive STB and CTB upon implantation. Consistent with the trophoderm, hPSC-TS^{CDX2} cells

do not form EVT cells under the differentiation conditions used for EVT differentiation of hPSC-TS and placenta-derived TS cells. Taken together, these results raise the question whether hPSC-TS^{CDX2} cells may be a more primitive cell type than hPSC-TS cells, analogous to the human trophoderm or simply a distinct cell type resulting from differences in cell culture conditions.

To investigate whether hPSC-TS^{CDX2} are similar to the human trophoderm, we compared transcriptome data for hPSC-TS, hPSC-TS^{CDX2}, and placenta-derived TS cells, with previously published data for trophoderm cells from human embryos (38). However, our analysis showed greater similarity in average expression levels among different TS cell types in culture than between hPSC-TS^{CDX2} and primary trophoderm cells; this is likely due to differences between cells in culture and primary human embryos, and experimental protocols for transcriptome analysis. Furthermore, blastocyst-derived TS cell lines and some TS cell lines derived from naïve human embryonic stem cells show defects in EVT differentiation (10). Therefore, further studies are needed to conclusively determine if hPSC-TS^{CDX2} cells are indeed similar to cells of the human trophoderm and/or represent a more primitive trophoblast cell type than hPSC-TS cells.

Considerations for derivation and culture of hPSC-TS^{CDX2} cells

To derive hPSC-TS^{CDX2} cells, undifferentiated hESCs maintained in E8 medium are first treated for 3 days with the S1PR3 agonist, BMP4 and the activin/nodal inhibitor SB4315432, to obtain *CDX2*⁺ cells. Subsequently, *CDX2*⁺ cells are passaged in TM4 medium to obtain hPSC-TS^{CDX2}. Using this protocol, we observed increased differentiation of H1 hESC-derived cells upon passage into TM4 medium, relative to H9 hESC- and SC102A-1 hiPSC-derived cells. Shortening the initial treatment step in case of H1 hESCs to 2 days eliminated excessive differentiation and facilitated derivation of hPSC-TS^{CDX2} cells. However, we were unable to derive

hPSC-TS^{CDX2} cells with hPSCs when the initial treatment was greater than 3 days.

It is important to note that hPSC-TS^{CDX2} cells proliferate slower in culture than hPSC-TS cells. They are passaged every 4-6 days at a 1:3-1:4 split ratio (as opposed to 1:4-1:6 for hPSC-TS cells). We also observe that the attachment of hPSC-TS^{CDX2} cells to tissue culture plates is less efficient than TS cells. Finally, we observe that excessive differentiation in TM4 medium during early passages could be countered by reducing the concentration of ascorbic acid (32 µg/mL instead of 64 µg/mL) in TM4. Additional studies on composition of TM4 medium or the substrates used to coat tissue culture plates may lead to improved growth rate and attachment efficiency. Alternatively, the slower growth rate and less efficient attachment characteristics may be an inherent feature of the hPSC-TS^{CDX2} state. Nonetheless, we have successfully maintained hPSC-TS^{CDX2} derived from all cell lines studied for at least 20 passages, in several independent runs over 5+ months. We recommend passaging hPSC-TS^{CDX2} cells routinely at higher cell densities relative to hPSC-TS cells, and troubleshooting cell line specific variability by optimizing the initial treatment step and/or lowering ascorbic acid concentration in TM4.

Derivation of hPSC-TS^{CDX2} and hPSC-TS cells from hiPSCs

We have shown that hPSC-TS^{CDX2} and hPSC-TS cells can be derived from hiPSCs. Since hiPSCs can be derived by reprogramming easily accessible somatic tissues, hPSC-TS and hPSC-TS^{CDX2} cells derived from hiPSCs can greatly accelerate research in placental biology. Further, arguably a limitation of blastocyst- or placenta-derived hPSC-TS cells is that pregnancy outcomes at term for the early gestation placental samples or blastocyst stage embryos used cannot be predicted accurately. In contrast, hiPSC-derived hPSC-TS and hPSC-TS^{CDX2}, from hiPSCs generated using somatic tissues obtained at term, will potentially enable development of models of validated normal and pathological trophoblast development. Pertinently, (6) have derived hiPSCs from

umbilical cords of normal pregnancies and those associated with early onset preeclampsia. Our results also gain particular significance in the light of restrictions on research with fetal tissue (45). However, while use of hiPSC-derived TS cells may shed light on the role of genetics in determining trophoblast pathology, reprogramming of somatic cells will likely alter their epigenome. Alteration of epigenetic signatures associated with placental pathology may limit the usefulness of these models. Thus, further research is needed to assess if TS cells derived from hiPSCs associated with placental pathology will retain disease phenotype.

In conclusion, using optimized cell culture protocols detailed in the current study, we have derived two distinct stem cell populations of the trophoctoderm lineage – hPSC-TS^{CDX2} and hPSC-TS – from human pluripotent stem cells. These stem cell models will be powerful tools for in vitro studies on human trophoblast development.

Experimental Procedures

Key Resources

Key resources used in this study are listed in **Table 1**

Culture of hPSCs

H1 and H9 hESCs and SC102A-1 hiPSCs were cultured on plates coated with vitronectin (5 µg/ml) at room temperature for at least one hour. Cells were cultured in 2 ml of TeSR-E8 medium at 37°C in 5% CO₂ in 6-well plates and culture medium was replaced every day. When cells reached confluency, they were passaged using ReLeSR according to the manufacturer's protocol, at a 1:10 split ratio.

Differentiation of hPSCs (6 days protocol)

The day after passaging, differentiation was initiated in hPSCs by treatment with S1P (10 µM), SB431542 (25 µM) and BMP4 (20 ng/ml) in TeSR-E7 for 6 days. In some experiments, the S1PR agonists CYM5442 hydrochloride (10 nM), CYM5520 (5 µM), or CYM5541 (2 µM) was added during the differentiation process. The medium was replaced every day. At day 6 of treatment, cells were dissociated with TrypLE for 5 min at 37°C. For differentiation to EVT, cells were seeded in a 6-well plate pre-coated with 5 µg/ml of vitronectin at a density of 7×10⁴ cells per well and cultured in 2 ml of EVT medium [TeSR-E8 medium supplemented with SB431542 (25 µM) and EGF (2.5 ng/ml)]. Medium was replaced every other day and analyzed at day 12 of total treatment. For differentiation to STB, cells were seeded in a 6-well plate pre-coated with 5 µg/ml of vitronectin at a density of 4×10⁴ cells per well and cultured in 2 ml of STB medium [TeSR-E6 supplemented with Activin A (20 ng/ml) and EGF (50 ng/ml)]. Medium was replaced every other day and analyzed at day 14 of total treatment.

Differentiation of hPSCs to hPSC-TS^{CDX2} and hPSC-TS cells

The day after passaging, hPSCs were differentiated by treatment with CYM5541 (2 µM), SB431542 (25 µM), BMP4 (20 ng/ml) in TeSR-E7 for 2 and 3 days for H1 and H9 hESCs, respectively. The medium was replaced every day. After 2 or 3 days of treatment, cells were dissociated with TrypLE for 5 minutes at 37°C. For propagation of hPSC-TS^{CDX2} cells, all cells were seeded in a 6-well plate pre-coated with 3 µg/ml of vitronectin and 1 µg/ml of Laminin 521 at a density of ~5×10⁴ cells per well and cultured in 2 ml of TM4 medium [TeSR-E6 medium supplemented with CYM5541 (2 µM), A 83-01 (0.5 µM), FGF10 (25 ng/ml) and CHIR99021 (2 µM)]. For establishment of hPSC-TS cells, all cells were seeded in a 6-well plate pre-coated with 3 µg/ml of vitronectin and 1 µg/ml of Laminin 521 at a density of ~5×10⁴ cells per well and cultured in 2 ml of TSCM developed by Okae et al. [DMEM/F12 supplemented with 0.1 mM 2-mercaptoethanol, 0.2% FBS, 0.5% Penicillin-Streptomycin, 0.3% BSA, 1% ITS-X supplement, 1.5 µg/ml L-ascorbic acid, 50 ng/ml EGF, 2 µM CHIR99021, 0.5 µM A83-01, 1 µM SB431542, 0.8 mM VPA and 5 µM Y27632](5). hPSC-TS^{CDX2} cells were directly passaged into TSCM for formation of hPSC-TS cells; complete transition took ~ 5 passages. Alternatively, hPSCs after 2 or 3 days of differentiation were directly passaged into TSCM.

Culture of hPSC-TS^{CDX2} and hPSC-TS cells

hPSC-TS^{CDX2} and hPSC-TS cells were cultured in TM4 and TSCM, respectively, in 2 ml of culture medium at 37°C in 5% CO₂. Culture medium was replaced every 2 days. When hPSC-TS^{CDX2} and hPSC-TS cells reached 70-90% confluency, they were dissociated with TrypLE at 37°C for 5-10 minutes and passaged to a new 6-well plate pre-coated with 3 µg/ml of vitronectin and 1 µg/ml of Laminin 521 at a 1:3-1:4 split ratio for hPSC-TS^{CDX2} and 1:4-1:6 split ratio for hPSC-TS cells. hPSC-TS^{CDX2} cells grown in TM4 medium were supplemented with Y-27632 upon passage to aid in single cell attachment. Cells were routinely passaged approximately every 4-6

days. hPSC-TS^{CDX2} and hPSC-TS cells at passages 5+ were used for analysis, with the exception of one replicate of H1-derived hPSC-TS^{CDX2} used in RNA-sequencing analysis where cells at passage 2 in TM4 were used.

Placenta-derived TS cells - CT30 (female) and CT29 (male), a kind gift from Drs. Hiroaki Okae and Takahiro Arima (Tohoku University, (5)) - were grown and passaged the same way in TSCM as hPSC-TS cells.

Differentiation of hPSC-TS^{CDX2} and hPSC-TS cells

hPSC-TS cells were grown to ~80-90% confluence in TSCM and dissociated with TrypLE for 10 min at 37°C. For differentiation to EVTs and STB, slightly modified versions of protocols developed by Okae et al. were used (5). For differentiation to EVTs, hPSC-TS cells were seeded in 6-well plates pre-coated with 3 µg/ml vitronectin and 1 µg/ml of Laminin 521 at a density of 1.25×10^5 cells per well and cultured in 2 mL of EVT medium (DMEM/F12 supplemented with 0.1 mM 2-mercaptoethanol, 0.5% Penicillin-Streptomycin, 0.3% BSA, 1% ITS-X supplement, 100 ng/ml NRG1, 7.5 µM A83-01, 2.5 µM Y27632, and 4% KSR). Matrigel was added to a final media concentration of 2% after suspending the cells in EVT medium. At day 3, the medium was replaced with the EVT medium without NRG1, and Matrigel was added to a final concentration of 0.5%. At day 6, cells were dissociated with TrypLE for 15 min at 37°C and passaged to a new vitronectin/laminin-coated 6-well plates at a 1:2 split ratio. The cells were suspended in the EVT medium without NRG1 and KSR. Matrigel was added to a final concentration of 0.5%, and cells were analyzed after two additional days of culturing. For differentiation to STB, cells were seeded in 6-well plates pre-coated 3 µg/ml vitronectin and 1 µg/ml of Laminin 521 at a density of 1.5×10^5 cells per well and cultured in 2 mL of DMEM/F12 supplemented with 0.1 mM 2-mercaptoethanol, 0.5% Penicillin-Streptomycin, 0.3% BSA, 1% ITS-X supplement, 2.5 µM Y27632, 2 µM forskolin, and 4% KSR. The medium was replaced at day 3, and cells were analyzed at day 6.

RNA Isolation, cDNA synthesis and Quantitative PCR.

RNA was isolated using TrizolTM reagent using the manufacturer's protocol. For cDNA synthesis, the RNA pellet was dissolved in diethyl pyrocarbonate (DEPC)-treated water. The RNA was purified using Baseline-ZERO DNase buffer and Baseline-ZERO DNase enzyme and incubating at 37°C for 30 min. The purification was stopped with Baseline-ZERO DNase stop solution and heated at 65°C for 10 min. cDNA was synthesized using 18-mer Oligo-dT and dNTP mix and heated to 65°C for 5 min and quickly chilled on ice. First strand buffer and DTT was added and incubated at 42°C for 2 min then superscript II RT enzyme was added and incubated at 42°C for 50 min. The enzyme was inactivated at 70°C for 15 min. The cDNA was stored at -20°C until further used. The Quantitative PCR (qPCR) reaction was carried out using SYBR Green Supermix in a C1000 Touch Thermal Cycler CFX384 Real-Time System (Bio-Rad). The primers used for qPCR analysis are listed in **Methods S1**. ANOVA analysis of gene expression data was carried out with SAS and package PCR in R software using the $\Delta\Delta C_t$ method to determine gene expression changes (46). QPCR analysis was carryout out using at least 3 biological replicates.

Immunofluorescence analysis

For immunofluorescence analysis, cells were grown on glass-bottom culture dishes coated with 3 µg/ml vitronectin and 1 µg/ml of Laminin 521. Cells were fixed either using 4% paraformaldehyde in PBS for 10 min, permeabilized with 0.5% Triton X-100 for 5 min and blocked in 3% BSA/PBS with 0.1% human IgG and 0.3% Triton X-100 for 1 hr. Cells were then incubated overnight with the primary antibody diluted in blocking buffer. The following primary antibodies were used: anti-KRT7 (SCB, 1:50), anti-KRT7 (CST, 1:500), rabbit anti-hCG (1:100), mouse anti-hCG (1:100), anti-YAP (1:200), anti-TFAP2C (1:400), anti-P63 (1:600), anti-GATA3 (1:500), anti-TEAD4 (1:250), anti-CDX2 (1:300), anti-VE-Cadherin (1:400), anti-HLA-G (1:300), anti-syncytin

(1:50). Corresponding isotype controls (rabbit polyclonal IgG, rabbit XP IgG, mouse IgG1, and mouse IgG2a) were used at primary antibody concentrations. Alexa Fluor 488- or Alexa Fluor 647-conjugated secondary antibodies were used as secondary antibodies. Nuclei were stained with DAPI and all samples were imaged using a Zeiss LSM 710 or 880 laser scanning confocal microscope (Carl Zeiss, Germany).

Confocal image analysis

Image analysis was conducted using an image processing algorithm created in MATLAB. First, the DAPI stain was isolated, binarized, and processed to accurately represent the number of cells in each image. The primary antibody stain of interest was isolated and processed in the same manner. Only primary antibody pixels that overlap DAPI pixels were considered for analysis, and the average intensities of those pixels were measured and correlated to the nearest nuclei. This was performed for one control image and multiple experimental images. Each cell in the experimental images was considered positively stained if the average intensity of that cell was greater than the average intensity of all cells in the control image. The average intensity of cells in the control image was subtracted from the average intensity for each individual cell across all images for each experimental condition to eliminate background. If no fluorescence signal was detected or if the average intensity was below the average intensity of the control image, then the expression for that cell was set to zero. The fraction of cells expressing a specific protein in each image was calculated as the ratio of the number of cells with non-zero fluorescence intensity to the total number of cells. Statistical analysis was done using a two-tailed t-test evaluating percent positive cells from different treatment groups.

Flow cytometry analysis

For flow cytometry analysis, cells were dissociated with TrypLE for 5 min at 37°C. Cells were fixed in suspension in 2% paraformaldehyde in PBS for 5 minutes at room temperature. Cells were permeabilized and blocked in 1% BSA/PBS with 1 mg/mL Saponin (Sigma 47036-50G-F) for 15 minutes at room temperature. Cells were then incubated for one hour on ice with the primary antibody diluted in the blocking buffer. The corresponding isotype control was used at the primary antibody concentration. Subsequently, cells were incubated in an Alexa Fluor 488-conjugated secondary antibody on ice protected from light for one hour and analyzed immediately in a 1% BSA/PBS buffer. A BD Accuri C6 Plus Flow Cytometer was used for analysis. Data from 10,000 events were collected.

RNA sequencing analysis using next generation sequencing

Total RNA was extracted with Trizol™ reagent using manufacturer's protocol. RNA from four biological replicates (i.e. cells from different passages) for cell line/type assessed was purified using GeneJET RNA Purification Kit using manufacturer's protocol. Isolated RNA samples were then used to evaluate genome-wide mRNA expression profiles using next generation RNA-sequencing, conducted at GENEWIZ, LLC. (South Plainfield, NJ, USA). RNA samples received at GENEWIZ were quantified using Qubit 2.0 Fluorometer (Life Technologies, Carlsbad, CA, USA) and RNA integrity was checked using Agilent TapeStation 4200 (Agilent Technologies, Palo Alto, CA, USA).

RNA sequencing libraries were prepared using the NEBNext Ultra RNA Library Prep Kit for Illumina following manufacturer's instructions (NEB, Ipswich, MA, USA). Briefly, mRNAs were first enriched with Oligo(dT) beads. Enriched mRNAs were fragmented for 15 minutes at 94 °C. First strand and second strand cDNAs were subsequently synthesized. cDNA fragments were end repaired and adenylated at 3'ends, and universal adapters were ligated to cDNA fragments, followed by index addition and library enrichment by limited-cycle PCR. The sequencing libraries

were validated on the Agilent TapeStation (Agilent Technologies, Palo Alto, CA, USA), and quantified by using Qubit 2.0 Fluorometer (Invitrogen, Carlsbad, CA) as well as by quantitative PCR (KAPA Biosystems, Wilmington, MA, USA).

The sequencing libraries were clustered on 4 lanes of a flowcell. After clustering, the flowcell was loaded on the Illumina HiSeq 4000 instrument according to manufacturer's instructions. The samples were sequenced using a 2x150bp Paired End (PE) configuration. Image analysis and base calling were conducted by the HiSeq Control Software (HCS). Raw sequence data (.bcl files) generated from Illumina HiSeq was converted into fastq files and de-multiplexed using Illumina's bcl2fastq 2.17 software. One mismatch was allowed for index sequence identification.

After investigating the quality of the raw data, sequence reads were trimmed to remove possible adapter sequences and nucleotides with poor quality using Trimmomatic v.0.36. The trimmed reads were mapped to the Homo sapiens GRCh38 reference genome available on ENSEMBL using the STAR aligner v.2.5.2b. The STAR aligner is a splice aligner that detects splice junctions and incorporates them to help align the entire read sequences. BAM files were generated as a result of this step. Unique gene hit counts were calculated by using feature Counts from the Subread package v.1.5.2. Only unique reads that fell within exon regions were counted.

Analysis of gene expression profiles

After extraction of gene hit counts, the gene hit counts table was used for downstream differential expression analysis. Genome-wide RNA sequencing count data were processed and statistically assessed using the DESeq2 package (v1.22.2) in R Software (3.6.0) (47). Count data were first filtered to include transcripts expressed above background, requiring the median across samples to be greater than the overall median signal intensity, as implemented in DESeq2. Count data were then normalized by median signal intensity using algorithms enabled within DESeq2, resulting in variance stabilized expression values (48). These normalized values were used to carry out a principal component analysis (PCA) comparing data-reduced global expression signatures across samples. Principal components were calculated and visualized using the prcomp function in R (49). The average gene expression levels of different cell types was compared using the Spearman rank correlation test. Transcriptome profiles obtained by single cell RNA sequencing of human embryos, and annotated as trophoctoderm (38), were combined for comparison with gene expression data from human trophoctoderm cells. Heat maps were generated using Partek® Genomics Suite Software (v7.18.0723) and gene-specific plots using GraphPad Prism Software (v8.2.0)), based on normalized expression values.

Statistical and gene set enrichment analysis of differentially expressed genes

Genes that showed the greatest difference in expression between the day 3 differentiated hESCs and undifferentiated hESCs, and hPSC-TS^{CDX2} and hPSC-TS cells were identified using an analysis of variance analysis (ANOVA) comparing the normalized expression levels between these two groups. Genes showing the greatest difference in expression between hPSC-TS^{CDX2} and hPSC-TS cells were identified using the following statistical filters: (1) a false discovery rate-corrected q-value<0.05 (50), and (2) a fold change in expression (ratio of average across hPSC-TS^{CDX2} and hPSC-TS cells samples) $\geq \pm 1.5$. To evaluate the biological role of these genes, a gene set enrichment analysis was carried out on the genes identified as significantly differentially expressed between groups. Specifically, all Gene Ontology (GO) gene sets (n=9996) from the Molecular Signature Database (MSigDB) (51) were queried for using the right-tailed Fisher's Exact test, as enabled through the 'platform for integrative analysis of omics data' (PIANO) packing in R (52). Gene sets were required to have an enrichment p-value<0.01 to be considered significant, consistent with previously published methods (53, 54). Genes that were identified at higher

expression levels were evaluated separately from genes identified at significantly lower expression levels in day 3 differentiated hESCs vs. undifferentiated hESCs, and hPSC-TS^{CDX2} vs. hPSC-TS cells.

Data availability

RNA sequencing data associated with this study has been deposited in Gene Expression Omnibus (GEO; accession number GSE137295). All other data that support the findings of this study are available within the article and its supplementary materials.

Author contributions

Conceptualization: AM and BR; Investigation: AM, VK, JM; Formal Analysis: AM, VK, BR, CC, JR, RF; Data curation: AM, BR, JR; Resources: ASM; Writing – original draft: AM and BR; Writing – review and editing: AM, BR, VK, JR, RF; Visualization: AM, VK, CC, JR; Project Administration: BR; Funding Acquisition: BR and ASM

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Conflict of interest

The authors declare that they have no conflicts of interest with the contents of this article.

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Table 1: Key resources

<i>REAGENT or RESOURCE</i>	<i>SOURCE</i>	<i>IDENTIFIER</i>
hPSC cell lines		
H1 hESCs	Wicell	RRID: CVCL_9771
H9 hESCs	Wicell	RRID: CVCL_9773
SC102A-1 hiPSCs	Systems Biosciences	RRID: CVCL_IT66
Antibodies and staining reagents		
Anti-KRT7	Santa Cruz Biotechnology	Cat#sc-23876, RRID:AB_2265604
Anti-KRT7	Cell Signaling Technologies	Cat# 4465, RRID:AB_11178382
Anti-hCG	Abcam	Cat# ab9582, RRID:AB_296507
Anti-hCG	Abcam	Cat# ab9376, RRID:AB_307221
Anti-P63	Cell Signaling Technologies	Cat# 13109, RRID:AB_2637091
Anti-GATA3	Cell Signaling Technologies	Cat# 5852, RRID:AB_10835690
Anti-TFAP2C	Cell Signaling Technologies	Cat# 2320, RRID:AB_2202287
Anti-YAP	Cell Signaling Technologies	Cat# 4912, RRID:AB_2218911
Anti-TEAD4	Abcam	Cat# ab58310, RRID:AB_945789
Anti-CDX2	Abcam	Cat# ab76541, RRID:AB_1523334
Anti-VE-Cadherin	Cell Signaling Technologies	Cat# 2500, RRID:AB_10839118
Anti-HLA-G	Abcam	Cat# ab52455, RRID:AB_880552
Anti-Syncytin	Santa Cruz Biotechnology	Cat# sc-50369, RRID:AB_2101536
Rabbit Polyclonal IgG	R&D Systems	Cat# AB-105-C, RRID:AB_354266
Rabbit XP IgG	Cell Signaling Technologies	Cat# 3900, RRID:AB_1550038
Mouse IgG1	Abcam	Cat# ab18447, RRID:AB_2722536
Mouse IgG2a	Abcam	Cat# 554126, RRID:AB_479661
Alexa Fluor 488-conjugated anti-rabbit IgG	Thermo Fisher Scientific	Cat# A-11034, RRID:AB_2576217
Alexa Fluor 647-conjugated anti-rabbit IgG	Thermo Fisher Scientific	Cat# A-21052, RRID:AB_2535719
DAPI	R&D Systems	Cat#5748
CellMask deep red plasma membrane stain	Invitrogen	Cat#C10046
Chemicals, Peptides, and Recombinant Proteins		
TrypLE	Thermo Fisher Scientific	Cat#12604013
Vitronectin	Thermo Fisher Scientific	Cat#A14700
Laminin 521	Stem Cell Technologies	Cat#77003
Human FGF-10	Stem Cell Technologies	Cat#78037
TeSR-E8	Stem Cell Technologies	Cat#05990
TeSR-E7	Stem Cell Technologies	Cat#05914
TeSR-E6	Stem Cell Technologies	Cat#05946
ReLeSR	Stem Cell Technologies	Cat#05872
Sphingosine-1-phosphate	Tocris	Cat#1370
D-erythro-dihydrosphingosine-1-phosphate	Abcam	Cat#ab141750
SB431542	Tocris	Cat#1614

BMP4	Thermo Fisher Scientific	Cat#PHC9534
CYM5442 hydrochloride	Tocris	Cat#3601
CYM5520	Tocris	Cat#5418
CYM5541	Tocris	Cat#4897
Y-27632 dihydrochloride	Tocris	Cat#1254
EGF	R&D Systems	Cat#236-EG
Doxycycline hyclate	Tocris	Cat#4090
Puromycin dihydrochloride	Tocris	Cat#4089
Activin A	R&D Systems	Cat#338-AC
Greiner Bio-one Cell View glass plates	Greiner Bio-one	Cat#627965
4% Paraformaldehyde in PBS	Thermo Fisher Scientific	Cat#R37814
Triton X-100	Sigma	Cat#T8787
PBS w/o CaMg	Sigma	Cat#D5773
PBS w/ CaMg	Sigma	Cat#D8662
Human IgG	Immunoreagents	Cat#Hu-003-C
BSA	Fisher Scientific	Cat#BP9703
10% BSA fatty acid free in PBS	Sigma	Cat#A1595
VPA	Sigma	Cat#P6273
A83-01	Tocris	Cat#2939
2-mercaptoethanol	Sigma	Cat#M3148
FBS	Thermo Fisher Scientific	Cat#16141-061
DMEM/F12	Thermo Fisher Scientific	Cat#11320033
ITS-X	Thermo Fisher Scientific	Cat#51500-056
L-ascorbic acid	Sigma	Cat#A8960
Pen/Strep	Thermo Fisher Scientific	Cat#15140122
Forskolin	Tocris	Cat#1099
Neuregulin	Cell Signaling Technologies	Cat#5218SC
Matrigel	Corning	Cat#354234
KSR	Thermo Fisher Scientific	Cat#10828028
Trizol Reagent	Thermo Fisher Scientific	Cat#15596018
DEPC	Sigma	Cat#95284
Baseline Zero DNAase Kit	VWR	Cat#76081-624
Oligo-dT	IDT	Cat#51-01-15-07
dNTP mix	Thermo Fisher Scientific	Cat#10297018
Superscript II RT	Thermo Fisher Scientific	Cat#18064014
SYBR Green Supermix	Bio-rad	Cat#1725272
Methanol	Fisher Scientific	Cat#A412-500
Acetone	Fisher Scientific	Cat#A18-500
Critical Commercial Kits		
GeneJET RNA Purification Kit	Thermo Fisher Scientific	Cat#K0731
Oligonucleotides		
qPCR Primers	IDT	Methods S1 for primer sequences
Software and Algorithms		

R (v3.6.0)	http://www.R-project.org/	N/A
DESeq2 package (v1.22.2)		
PCR package (v1.2.2)		
SAS Software		N/A
Zeiss Zen Software	https://www.zeiss.com/microscopy/us/products/microscope-software/zen-lite.html	N/A

Figure legends

Figure 1: A chemically defined medium containing S1P enables differentiation of hESCs to CTB-like cells and terminally differentiated trophoblasts.

(A) Schematic of protocol for hESC differentiation to trophoblast.

(B) Confocal images of CTB from 6-day initial treatment of H9 hESCs, staining for KRT7, P63, GATA3, and CDX2. Nuclei were stained with DAPI.

(C) Confocal images of EVT from 12-day treatment of H9 hESCs, staining for KRT7, HLA-G and VE-Cadherin. Nuclei were stained with DAPI.

(D) Confocal images of STB from 14-day treatment of H9 hESCs, staining for KRT7 and hCG, and syncytin. Nuclei were stained with DAPI. Membrane was stained with CellMask deep red plasma membrane stain.

(E) Confocal images of cells from 12-day EVT treatment of H9 hESCs upon removal of S1P, staining for HLA-G and VE-Cadherin. Nuclei were stained with DAPI.

(F) Confocal images of cells from 14-day STB treatment of H9 hESCs upon removal of S1P, staining for KRT7 and syncytin. Nuclei were stained with DAPI.

Scale bars are 100µm for all images.

Figure 2: S1P mediates its effects on trophoblast differentiation of hESCs through its receptors.

(A) Confocal images of CTB from 6-day treatment of H9 hESCs using D-erythro-dihydrospingosine-1-phosphate (dhS1P), CYM5442 (S1PR1 agonist), CYM5220 (S1PR2 agonist), and CYM5541 (S1PR3 agonist), staining for CDX2, GATA3, P63, and TEAD4. Nuclei were stained with DAPI.

(B) Confocal images of STB from 14-day treatment of H9 hESCs using dhS1P, CYM5442, CYM5520, and CYM5541 during initial 6-day treatment, staining for KRT7 and hCG. Nuclei were stained with DAPI.

(C) Confocal images of EVT from 12-day treatment of H9 hESCs using dhS1P, CYM5442, CYM5220, and CYM5541 during initial 6-day treatment, staining for HLA-G and VE-Cadherin. Nuclei were stained with DAPI.

Scale bars are 100µm for all images.

Figure 3: Optimizing timing of hESC differentiation enables derivation of hPSC-TS^{CDX2} cells.

(A) Schematic of differentiation protocol for establishment of hPSC-TS^{CDX2} and hPSC-TS from hESCs.

(B) Confocal images of 3-day treated H9 and H1 hESCs, staining for CDX2, P63, and TEAD4. Nuclei were stained with DAPI. Scale bars are 100µm.

(C) Confocal images of 6-day treated H9 and H1 hESCs, staining for CDX2. Nuclei were stained with DAPI. Scale bars are 100 µm.

(D) Quantitative analysis of cells expressing nuclear CDX2 after 3-day and 6-day differentiation treatment of H1 (day 3, 5455 cells in 3 images; day 6, 2448 cells in 2 images) and H9 (day 3, 5552 cells in 4 images; day 6, n=6448 cells in 5 images) hESCs. Data points represent fraction of CDX2⁺ cells in individual images from at least two biological replicates. Analysis was performed in MATLAB and at least two biological replicates were used. (Error bars are S.D., ***p<0.05).

- (E) Confocal images of H9 hPSC-TS^{CDX2} in TM4, staining for CDX2, TFAP2C, GATA3, YAP, TEAD4, and P63. Nuclei were stained with DAPI. Scale bars are 200 μ m.
- (F) Confocal images of STB from H9 hPSC-TS^{CDX2} staining for hCG and KRT7. Nuclei were stained with DAPI. Scale bars are 100 μ m.
- (G) Confocal images of EVT from H9 hPSC-TS^{CDX2}, staining for HLA-G (red) and VE-Cadherin (green) as well as KRT7 (red) and hCG (green). Nuclei were stained with DAPI. Scale bars are 200 μ m.

Figure 4: Formation of hPSC-TS cells.

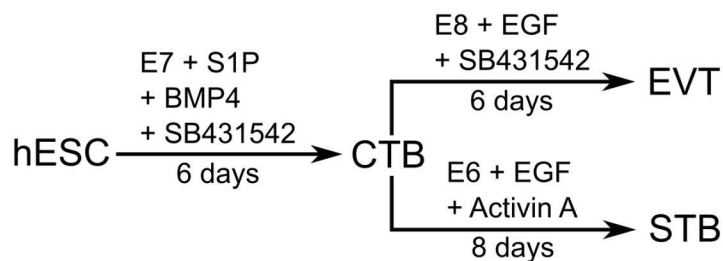
- (A) Confocal images of H9 hPSC-TS in TSCM, staining for CDX2, TFAP2C, GATA3, YAP, TEAD4, and P63. Nuclei were stained with DAPI. Scale bars are 200 μ m.
- (B) Flow cytometry histogram of KRT7 expression of H9 hPSC-TS cells in TSCM compared to an isotype control.
- (C) Confocal images of EVT from H9 hPSC-TS cells, staining for HLA-G and VE-Cadherin. Nuclei were stained with DAPI. Scale bars are 200 μ m.
- (D) Flow cytometry histogram of HLA-G expression of EVT from H9 hPSC-TS cells compared to an isotype control.
- (E) Gene expression of *CG β* , *SDC1*, *CSH1/2*, *HLA-G*, *MMP2*, *TEAD4*, and *TP63* of EVT from H9 hPSC-TS- and placenta-derived TS #1 (CT30) and TS #2 (CT29) cells. Four biological replicates were used. (Error bars, S.E., * $p < 0.05$ from TS cells).
- (F) Confocal images of STB from H9 hPSC-TS, staining for hCG and KRT7. Nuclei were stained with DAPI. Scale bars are 100 μ m.
- (G) Gene expression of *CG β* , *SDC1*, *CSH1/2*, *HLA-G*, *MMP2*, *TEAD4*, and *TP63* of STB from H9 hPSC-TS and placenta-derived TS #1 (CT30) and TS #2 (CT29) cells. Four biological replicates were used. (Error bars, S.E., * $p < 0.05$ from TS cells).

Figure 5: Transcriptome analysis confirms equivalence of hESC-derived and primary TS cells and reveal differences between hPSC-TS and hPSC-TS^{CDX2}

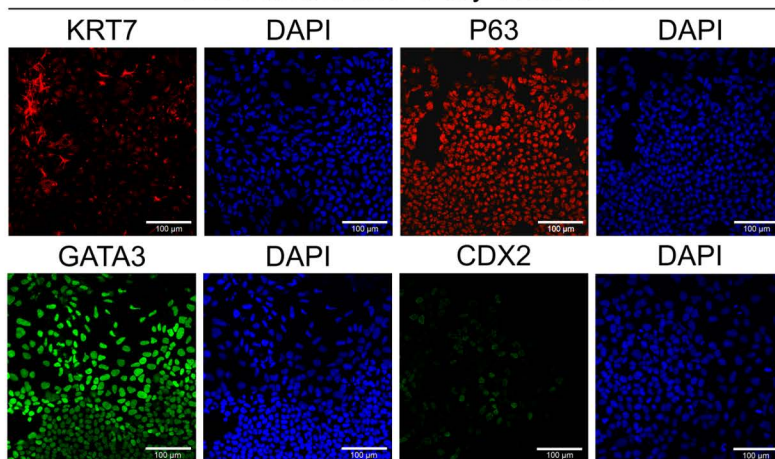
- (A) Principal component analysis (PCA) of transcriptome data on H1 and H9 hESCs, H1 and H9 hESCs after 3-day treatment, H1 and H9 hESC-derived hPSC-TS^{CDX2} cultured in TM4, H1 and H9 hESC-derived hPSC-TS and placenta-derived TS #1 (CT30) and TS #2 (CT29) cultured in TSCM.
- (B) Spearman correlation coefficients for comparison between hESCs (H1 and H9), hESC after 3-day treatment (H1 and H9), hESC-derived hPSC-TS^{CDX2} cultured in TM4, hESC-derived hPSC-TS (H1 and H9) and placenta-derived TS #1 (CT30) and TS #2 (CT29) cultured in TSCM ($p < 0.00001$).
- (C) Hierarchical clustering analysis of transcriptome data from H1 and H9 hESC-derived hPSC-TS and placenta-derived TS #1 (CT30) and TS #2 (CT29). Four biological replicates (i.e. cells from different passages) were used.
- (D) Relative expression of trophoblast-associated markers *CDX2* and *HAND1* and villous CTB-associated marker *TP63* in hESC-derived hPSC-TS^{CDX2} and hPSC-TS (H1 and H9) (* $q < 0.001$).

Figure 6: hPSC-TS^{CDX2} and hPSC-TS generated from hiPSCs.

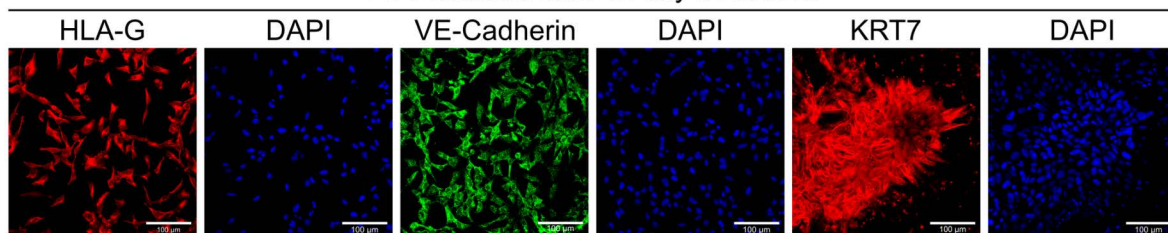
- (A) Confocal image of SC102A-1 hPSC-TS^{CDX2} in TM4, staining for CDX2, TFAP2C, GATA3, YAP, TEAD4, and P63. Nuclei were stained with DAPI. Scale bars are 200µm.
- (B) Confocal images of SC102A-1 hPSC-TS in TSCM, staining for CDX2, TFAP2C, GATA3, YAP, TEAD4, and P63. Scale bars are 200µm.
- (C) Flow cytometry histogram of KRT7 expression of SC102A-1 hPSC-TS cells in TSCM compared to an isotype control.
- (D) Proliferation of SC102A-1 hPSC-TS, placenta-derived TS #1 (CT30), and TS #2 (CT29) in TSCM. 1×10^5 cells were seeded and cells were counted after 3 days. Four biological replicates were used. (Error bars, S.D.)
- (E) Flow cytometry histogram of HLA-G expression of EVTs from SC102A-1 hPSC-TS cells compared to an isotype control.
- (F) Gene expression of *CGβ*, *SDC1*, *CSH1/2*, *HLA-G*, *MMP2*, *TEAD4*, and *TP63* of EVTs compared to TS cells from SC102A-1 hPSC-TS and placenta-derived TS #1 (CT30) and TS #2 (CT29). Four biological replicates were used. (Error bars, S.E., * $p < 0.05$ for differential expression relative to TS cells). Data for placenta-derived TS cells is the same as used in Figure 4.
- (G) Confocal images of EVTs from SC102A-1 hPSC-TS, staining for HLA-G and VE-Cadherin. Scale bars are 100µm.
- (H) Gene expression of *CGβ*, *SDC1*, *CSH1/2*, *HLA-G*, *MMP2*, *TEAD4*, and *TP63* of STBs compared to TS cells from SC102A-1 hPSC-TS and placenta-derived TS #1 (CT30) and TS #2 (CT29). Four biological replicates were used. (Error bars, S.E., * $p < 0.05$).
- (I) Confocal images of STB from SC102A-1 hPSC-TS, staining for hCG and KRT7. Scale bars are 100µm.

A**B**

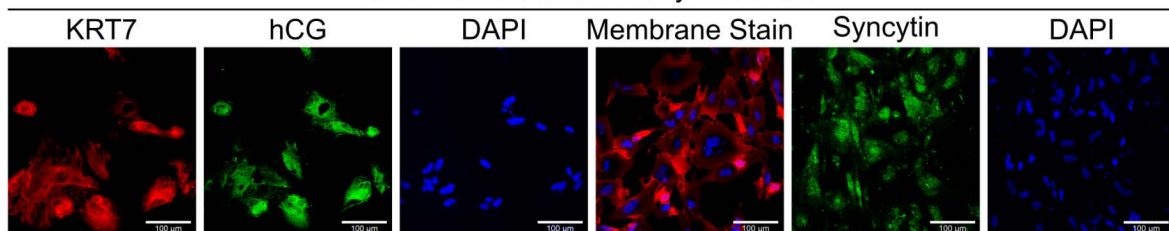
CTB markers after 6 day treatment

**C**

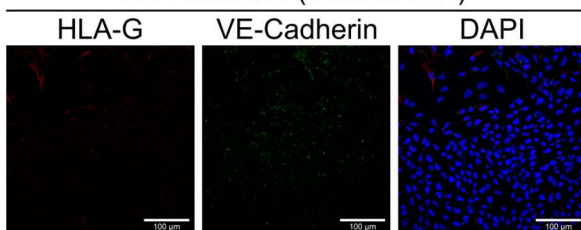
EVT markers after 12 day treatment

**D**

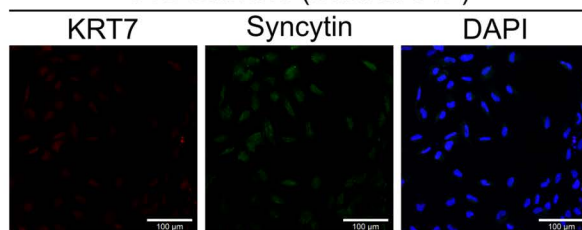
STB markers after 14 day treatment

**E**

EVT markers (without S1P)

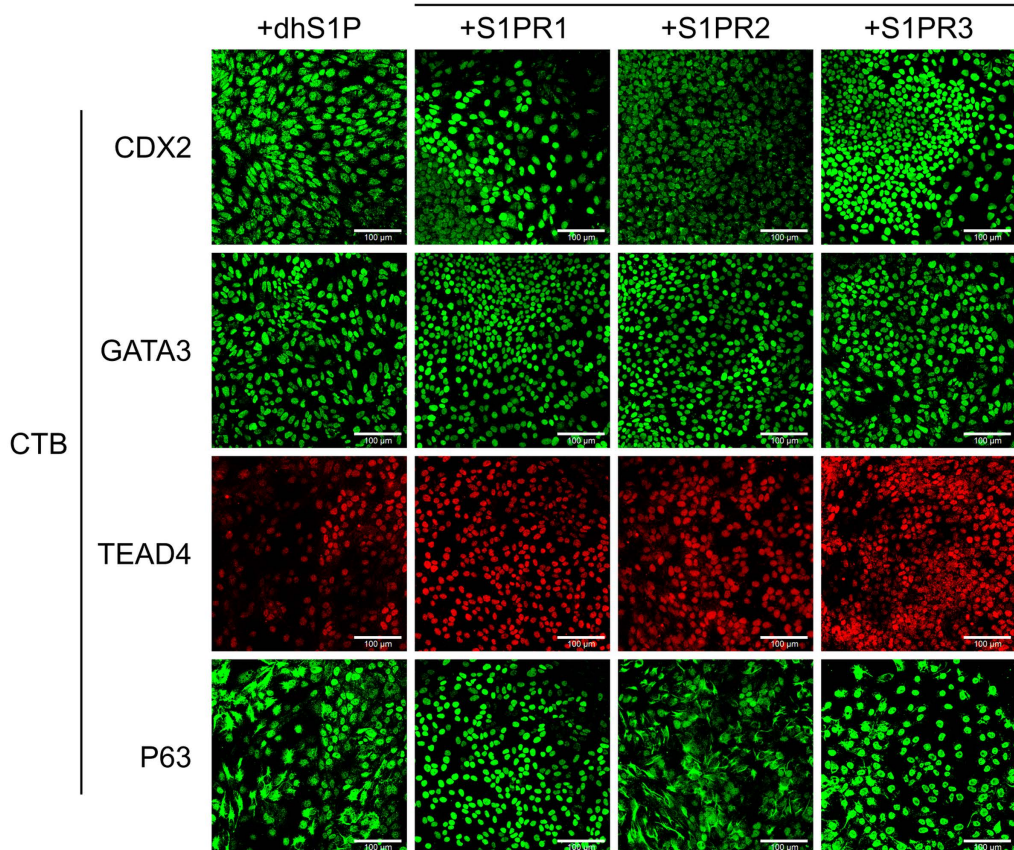
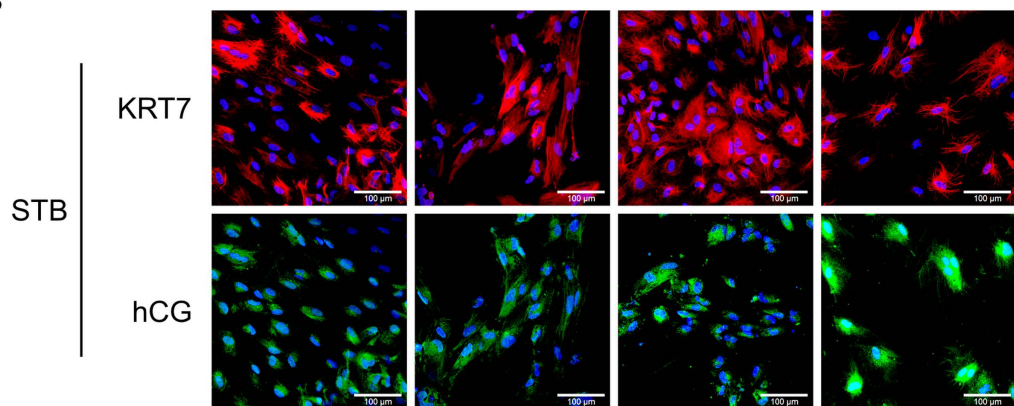
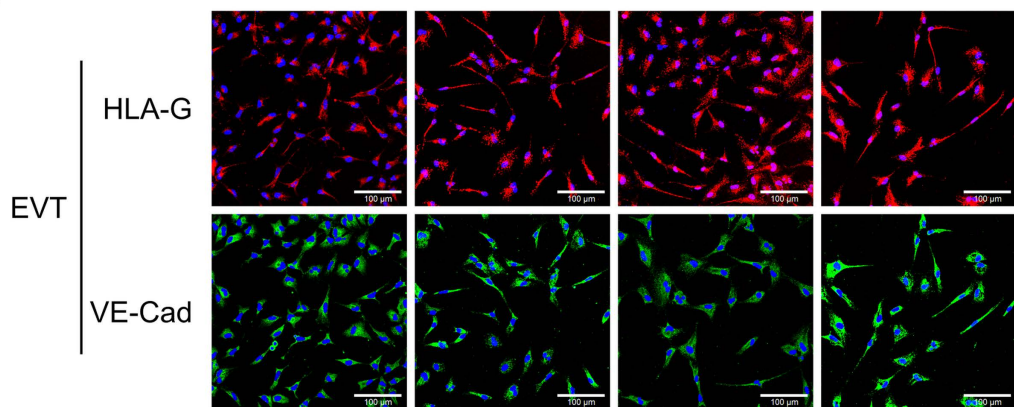
**F**

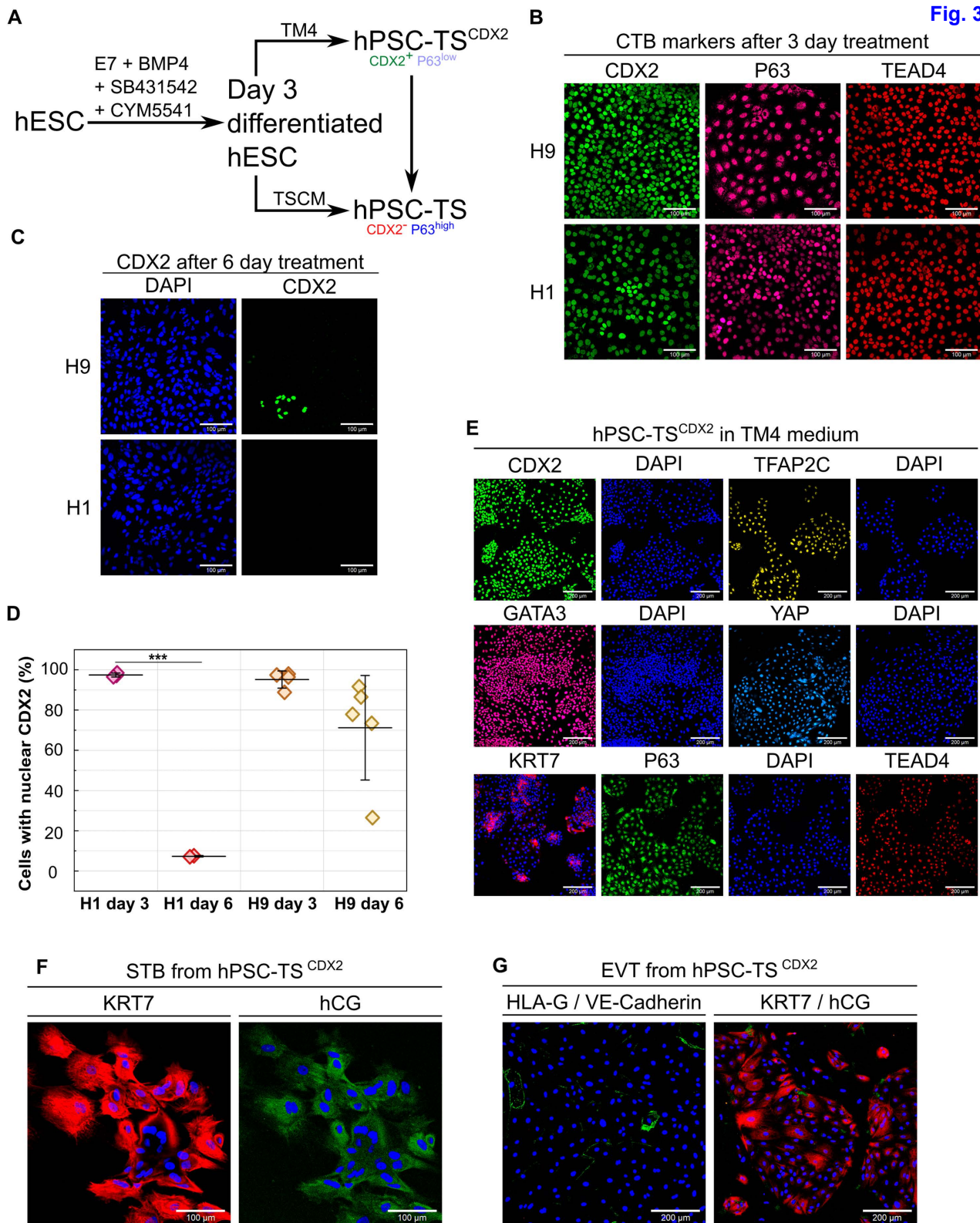
STB markers (without S1P)



A

Agonist for:

Fig. 2**B****C**



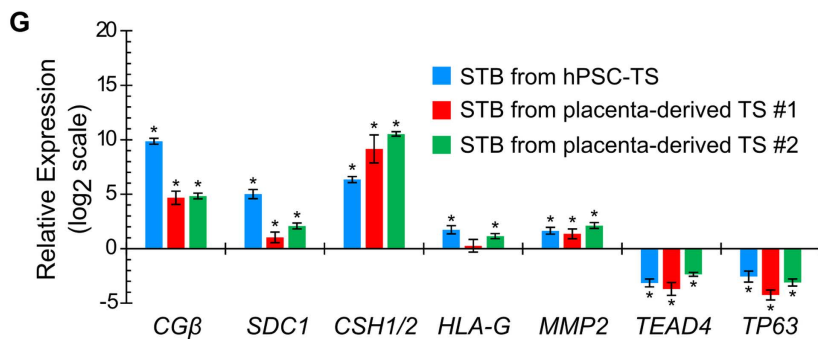
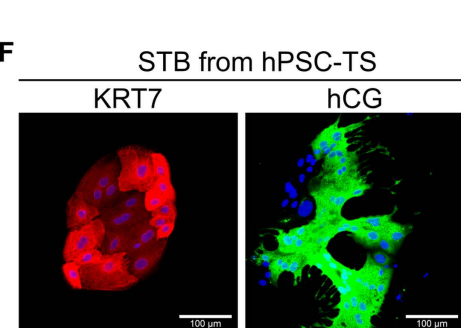
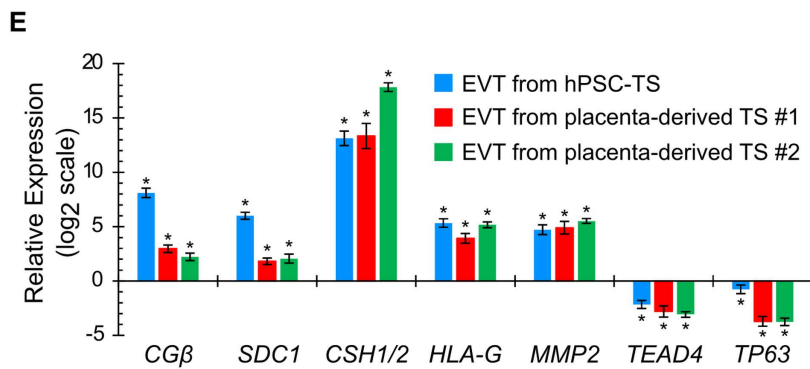
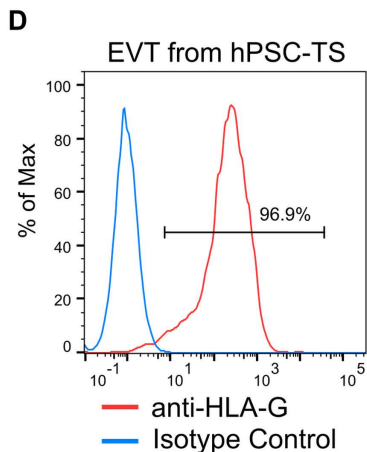
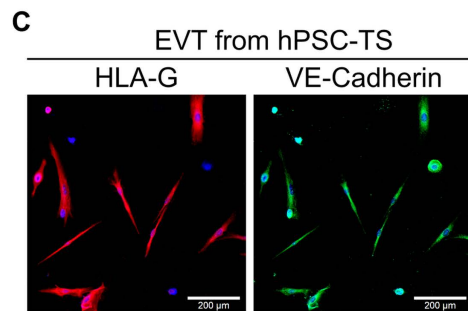
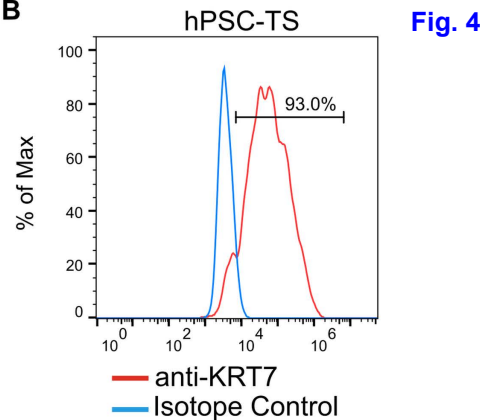
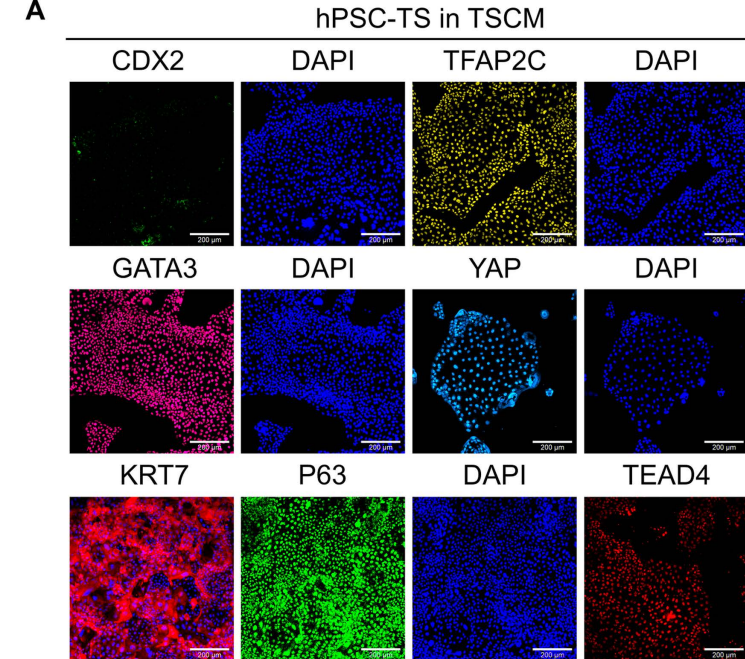
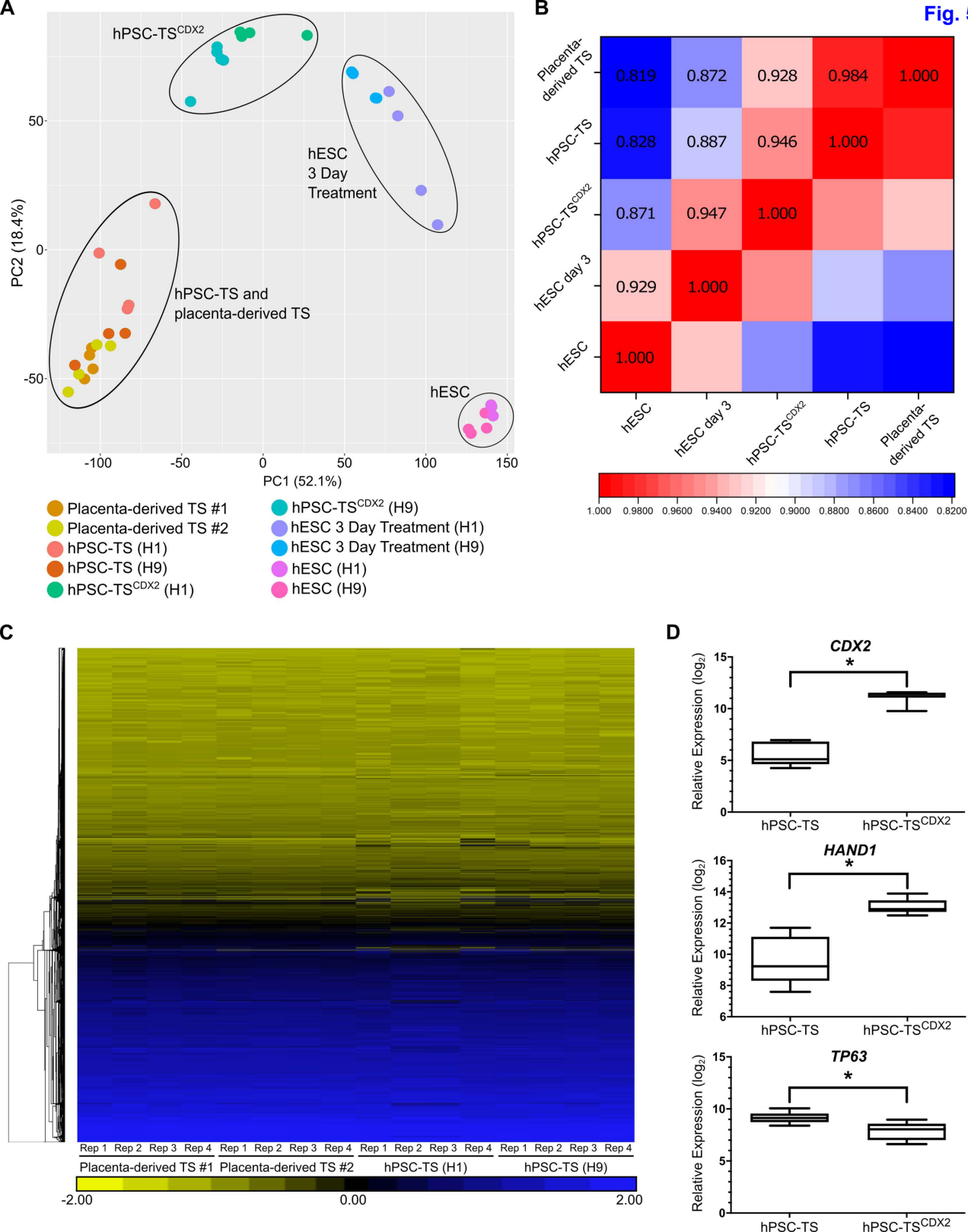
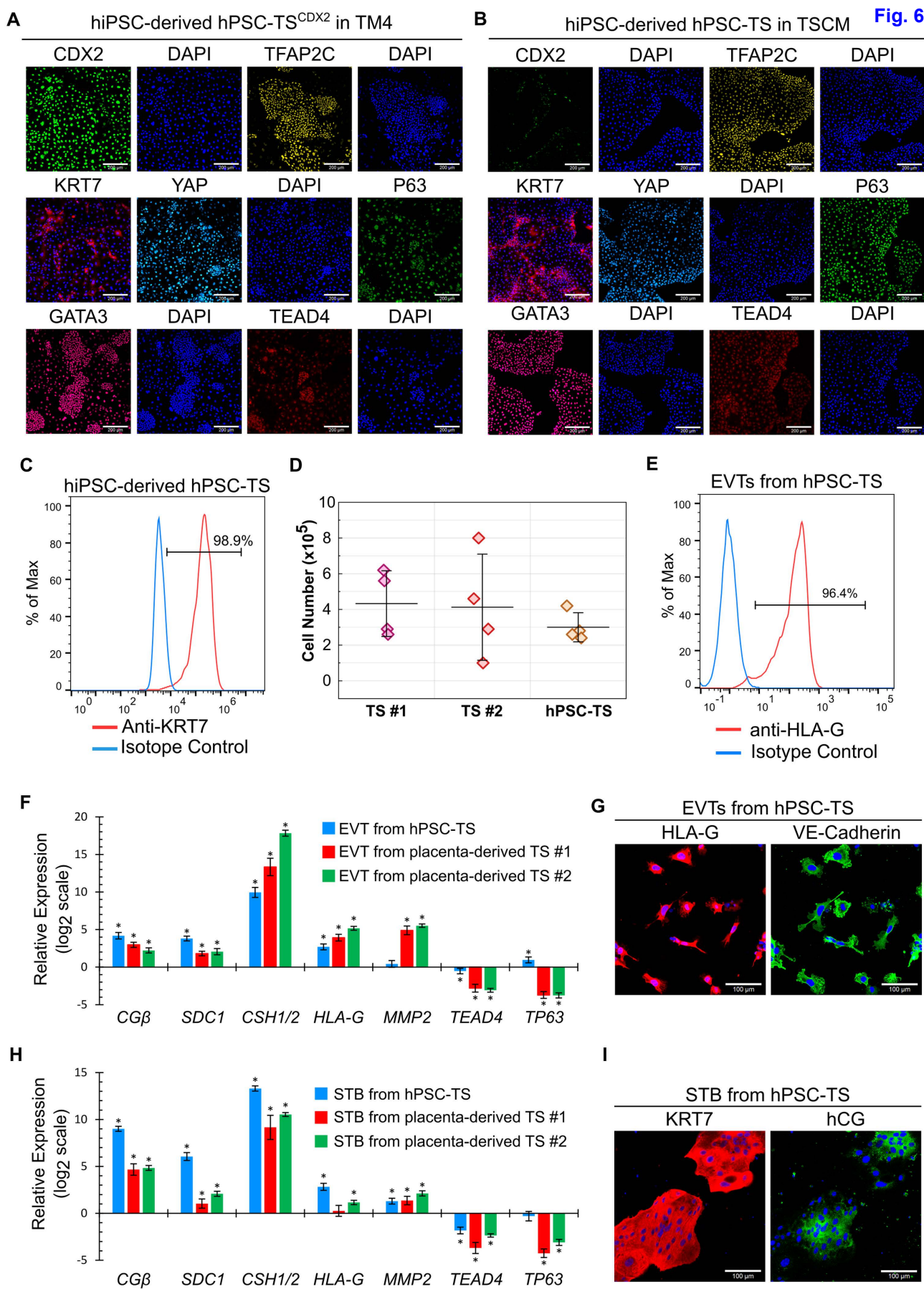


Fig. 5





Supplemental Information

Two distinct trophectoderm lineage stem cells from human pluripotent stem cells

Adam Mischler¹, Victoria Karakis¹, Jessica Mahinthakumar¹, Celeste K. Carberry², Adriana San Miguel¹, Julia E. Rager², Rebecca C. Fry², Balaji M. Rao^{1,3*}

¹Department of Chemical and Biomolecular Engineering, North Carolina State University, Raleigh, North Carolina 27695, USA

²Department of Environmental Sciences and Engineering, Institute for Environmental Health Solutions, University of North Carolina - Chapel Hill, Chapel Hill, North Carolina 27599, USA

³Golden LEAF Biomanufacturing Training and Education Center (BTEC), North Carolina State University, Raleigh, North Carolina 27695, USA

*Corresponding author: Email: bmrao@ncsu.edu

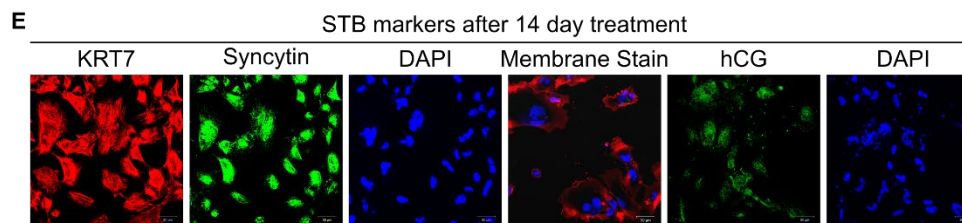
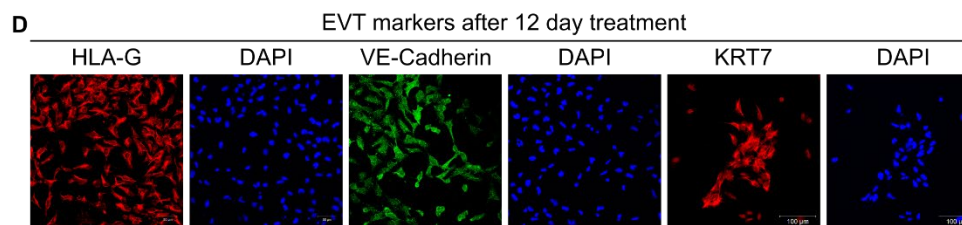
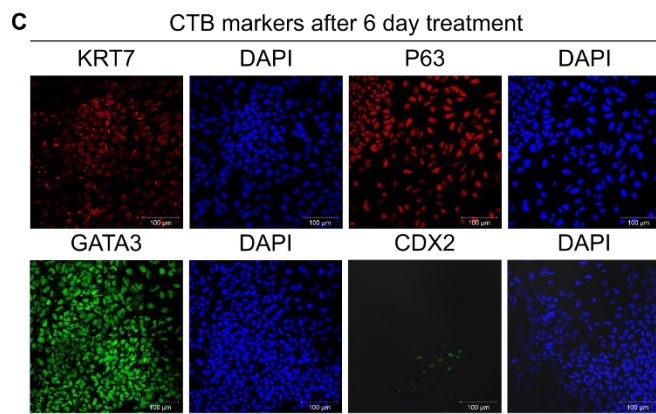
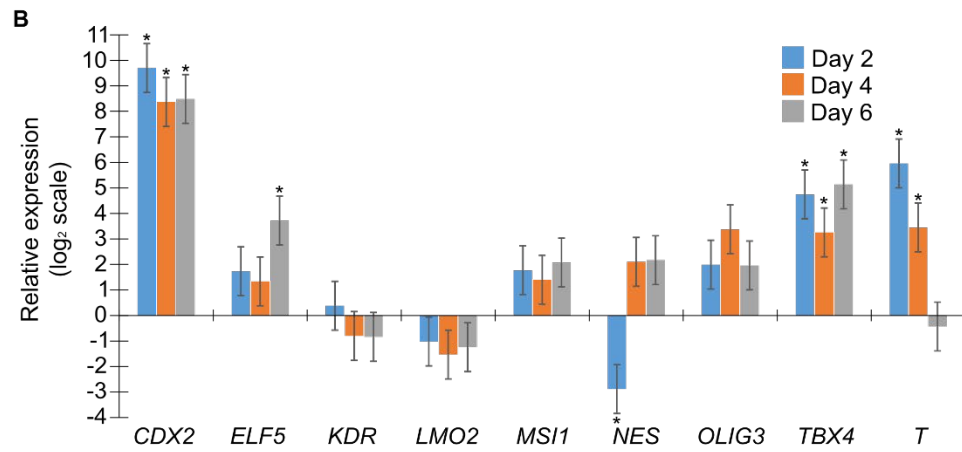
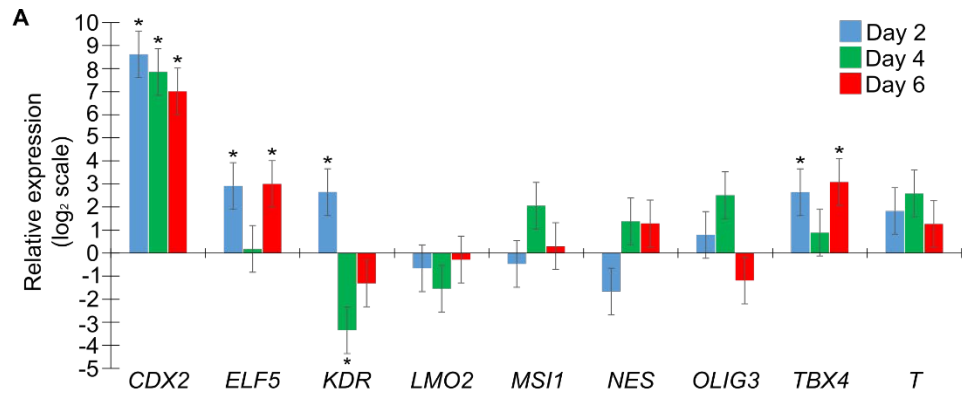


Figure S1: A chemically defined medium containing S1P enables differentiation of hESCs to CTB and terminally differentiated trophoblasts. Related to Figure 1.

(A) Gene expression of CTB: *CDX2*, *ELF5*; Mesoderm: *KDR*, *LMO2*, *T* (brachyury), *TBX4* and neural genes: *MSH1*, *NES* (nestin), *OLIG3* in H9 hESCs undergoing differentiation, compared to hESCs. Three biological replicates were used. (Error bars, S.E., * $p < 0.05$).

(B) Gene expression of CTB: *CDX2*, *ELF5*; Mesoderm: *KDR*, *LMO2*, *T* (brachyury), *TBX4* and neural genes: *MSH1*, *NES* (nestin), *OLIG3* in H1 hESCs undergoing differentiation compared to hESCs. Three biological replicates were used. (Error bars, S.E., * $p < 0.05$).

(C) Confocal images of CTB from 6-day initial treatment of H1 hESCs, staining for KRT7, P63, GATA3, and CDX2. Nuclei were stained with DAPI.

(D) Confocal images of EVT from 12-day treatment of H1 hESCs, staining for KRT7, HLA-G and VE-Cadherin. Nuclei were stained with DAPI.

(E) Confocal images of STB from 14-day treatment of H1 hESCs, staining for KRT7, syncytin and hCG. Nuclei were stained with DAPI. Membrane was stained with CellMask deep red plasma Membrane stain.

Scale bars are 100 μ m for all images.

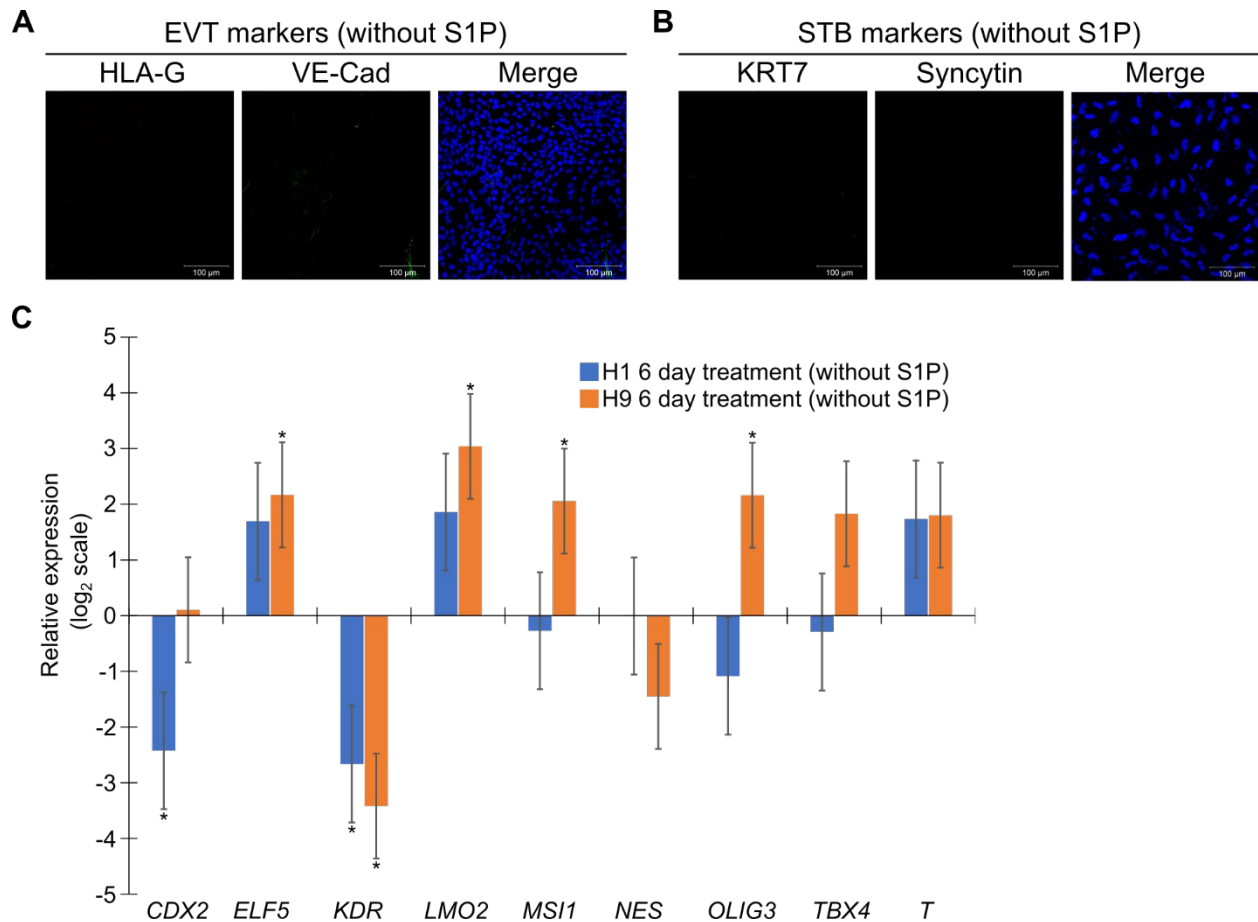


Figure S2: Exogenous S1P is necessary for differentiation of hESCs to trophoblast in chemically defined medium. Related to Figure 1.

(A) Confocal images of cells from 12-day EVT treatment of H1 hESCs upon removal of S1P, staining for HLA-G and VE-Cadherin. Nuclei were stained with DAPI.

(B) Confocal images of cells from 14-day STB treatment of H1 hESCs upon removal of S1P staining for KRT7 and syncytin. Nuclei were stained with DAPI.

(C) Gene expression of *CDX2*, *ELF5*, *KDR*, *LMO2*, *MSH1*, *NES* (nestin), *OLIG3*, and *T* (brachyury) in 6-day treatment of H9 and H1 hESCs upon removal of S1P, compared to 6-day treatment in the presence of S1P. Three biological replicates were used. (Error bars are S.E., * $p < 0.05$)

Scale bars are 100 μ m for all images.

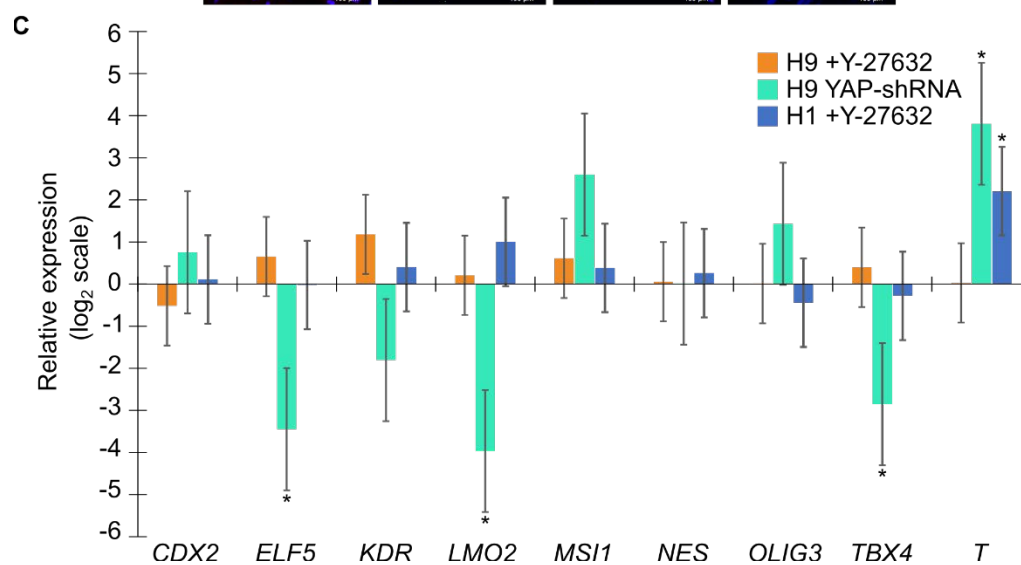
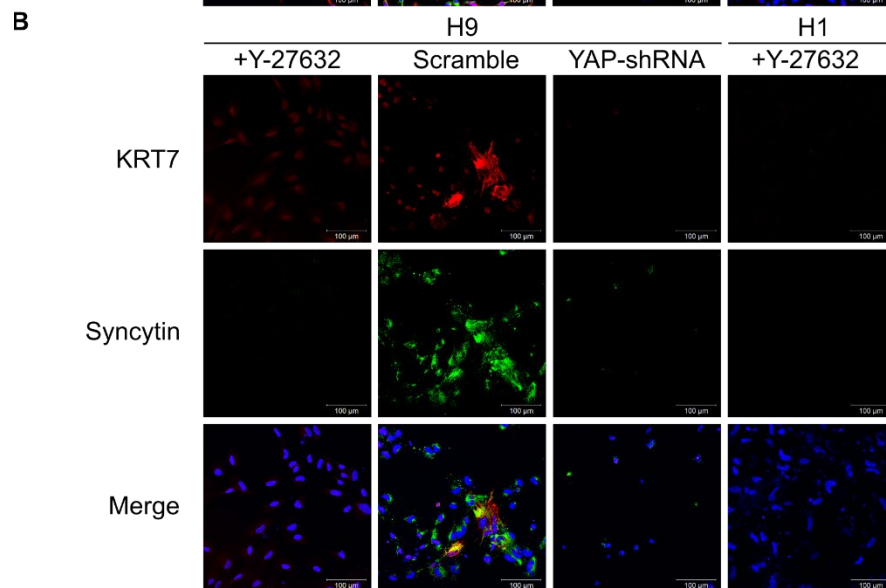
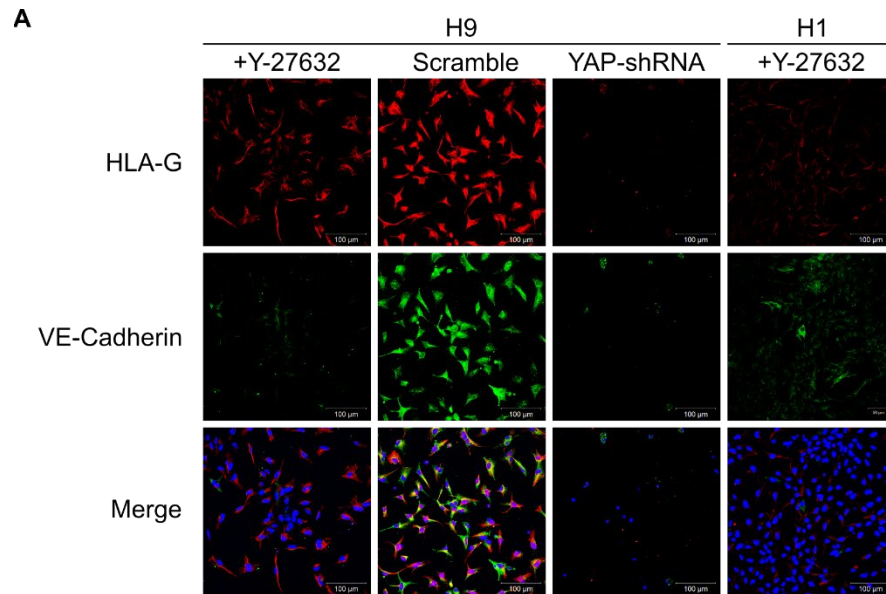


Figure S3: Rho/Rock signaling and YAP are necessary for differentiation of hESCs to trophoblast in chemically defined medium. Related to Figure 1

(A) Confocal images of cells from 12-day EVT treatment of H9 and H1 hESCs with the addition of ROCK inhibitor (+Y-27632), knockdown of YAP using an inducible shRNA (YAP-shRNA), or a scrambled shRNA control (scramble), staining for HLA-G and VE-Cadherin. Nuclei were stained with DAPI.

(B) Confocal images of cells from 14-day STB treatment of H9 and H1 hESCs with addition of ROCK inhibitor (+Y-27632), knockdown of YAP using an inducible shRNA (YAP-shRNA), or a scrambled shRNA control (scramble), staining for KRT7 and syncytin. Nuclei were stained with DAPI.

(C) Gene expression of *CDX2*, *ELF5*, *KDR*, *LMO2*, *MSH1*, *NES* (nestin), *OLIG3*, and *T* (brachyury) in H9 and H1 hESCs undergoing differentiation with the addition of ROCK inhibitor (+Y-27632) and knockdown of YAP using an inducible shRNA (YAP-shRNA), compared to the 6-day time point in the presence of S1P or scrambled shRNA knockdown in presence of S1P. Three biological replicates were used. (Error bars are S.E., * $p < 0.05$)

Scale bar is 100 μ m for all images.

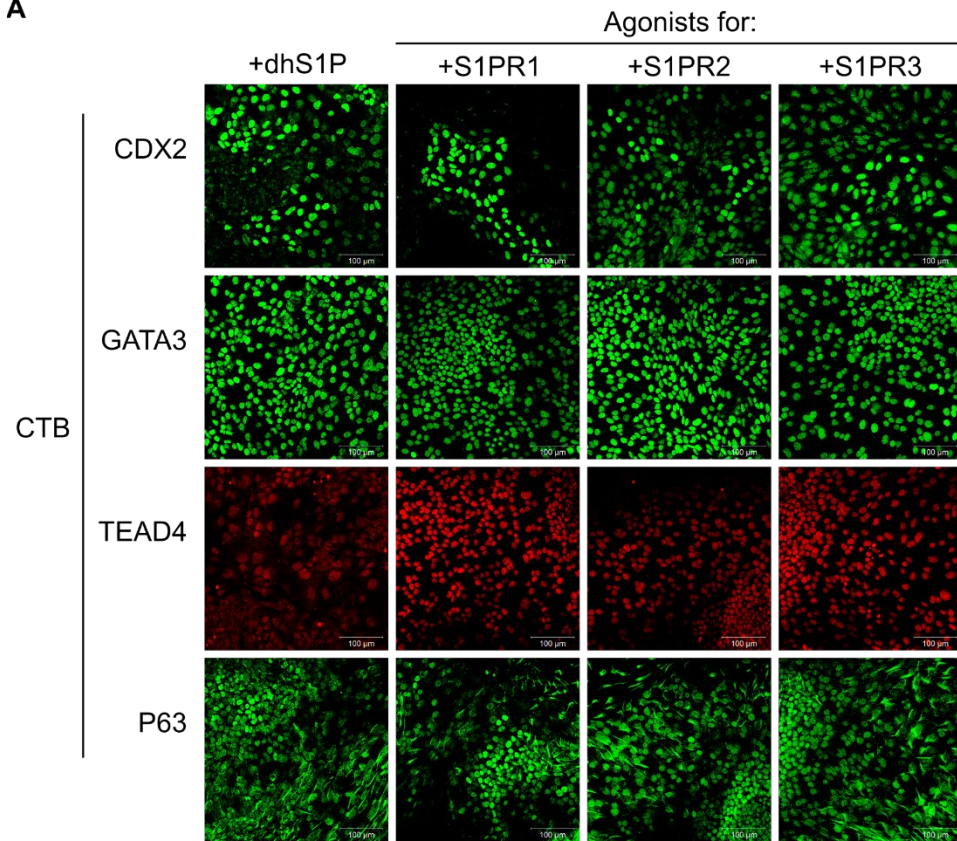
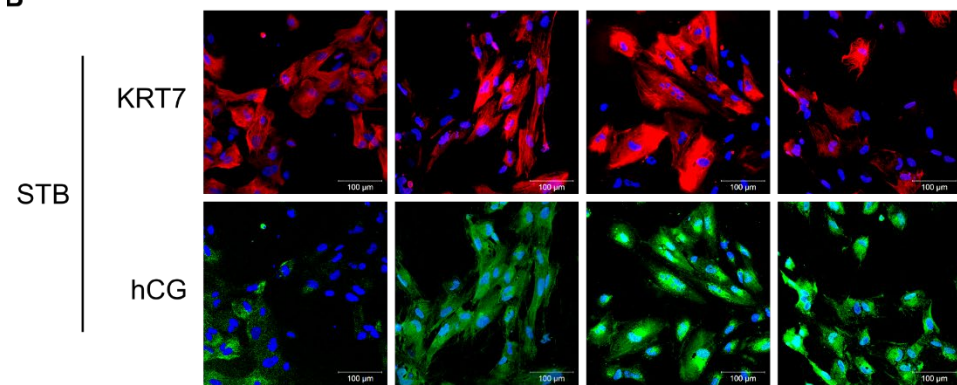
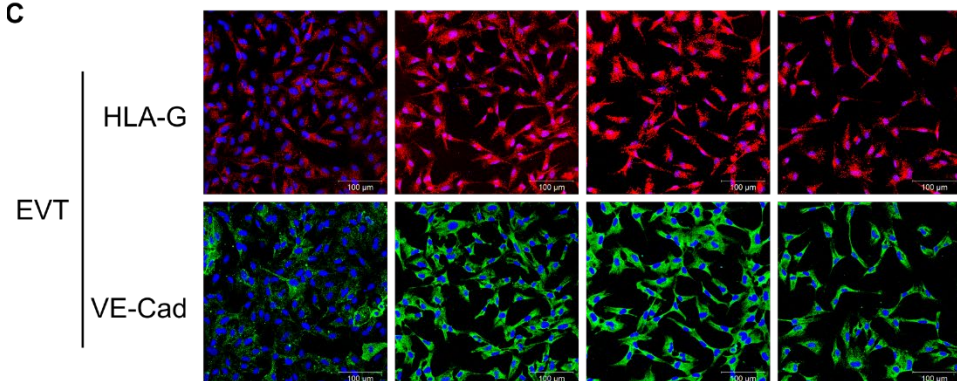
A**B****C**

Figure S4: S1P mediates its effects on trophoblast differentiation of hESCs through its receptors. Related to Figure 2.

(A) Confocal images of CTB from 6-day treatment of H1 hESCs using D-erythro-dihydrospingosine-1-phosphate (dhS1P), CYM5442 (S1PR1 agonist), CYM5220 (S1PR2 agonist), and CYM5541 (S1PR3 agonist), staining for CDX2, GATA3, P63, and TEAD4. Nuclei were stained with DAPI.

(B) Confocal images of STB from 14-day treatment of H1 hESCs using dhS1P, CYM5442, CYM5520, and CYM5541 during initial 6-day treatment, staining for KRT7 and hCG. Nuclei were stained with DAPI.

(C) Confocal images of EVT from 12-day treatment of H1 hESCs using dhS1P, CYM5442, CYM5220, and CYM5541 during initial 6-day treatment, staining for HLA-G and VE-Cadherin. Nuclei were stained with DAPI.

Scale bars are 100µm for all images.

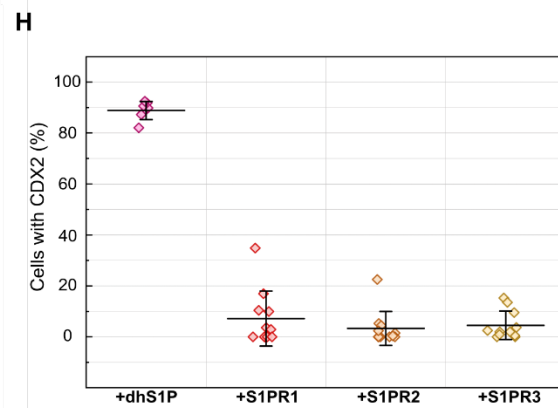
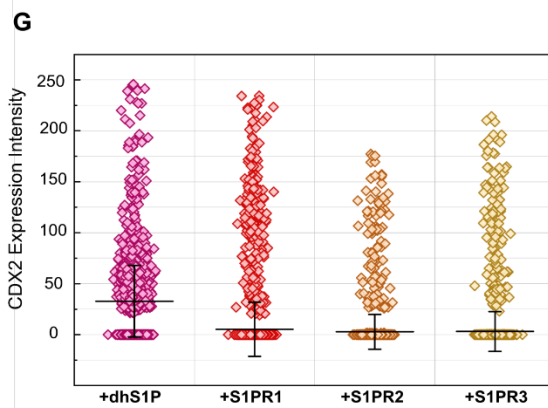
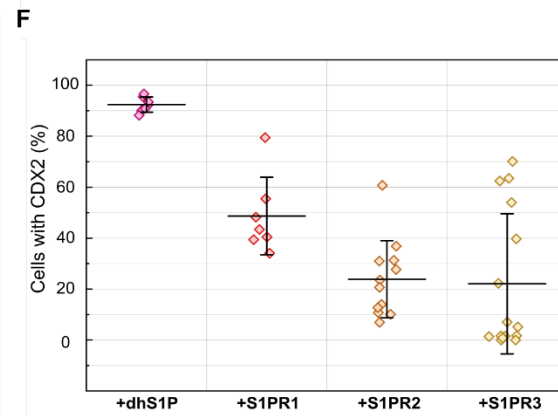
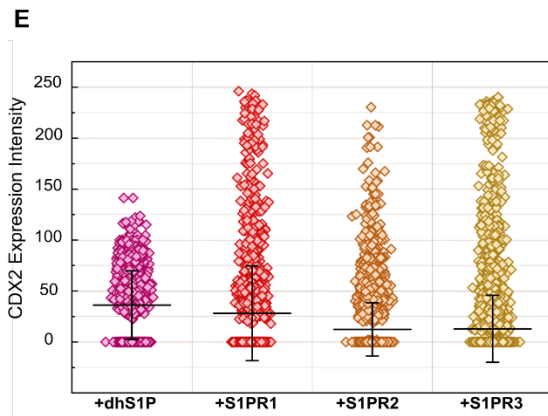
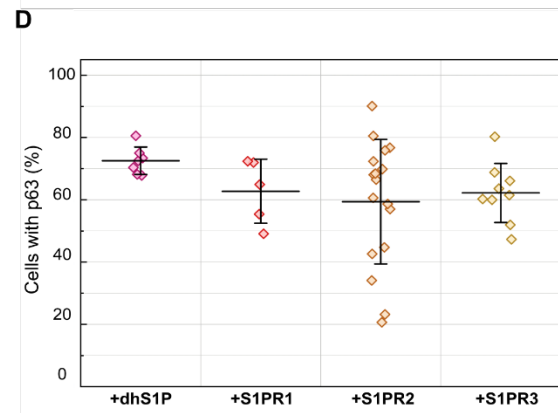
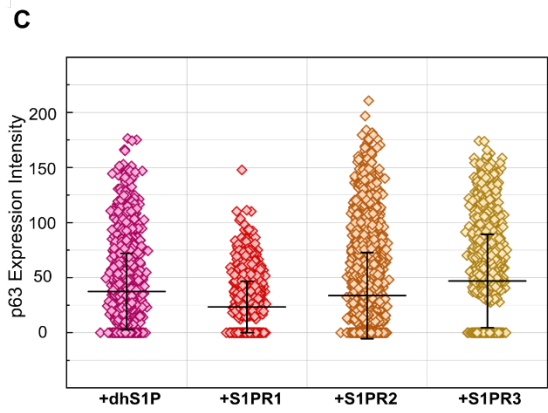
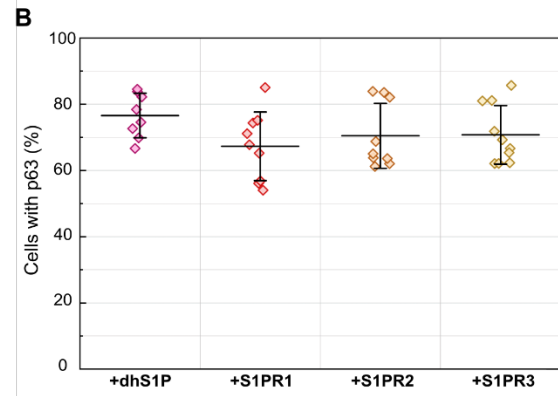
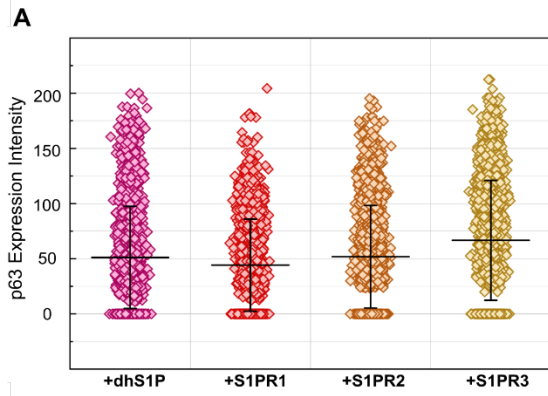


Figure S5: S1P mediates its effects on trophoblast differentiation of hESCs through its receptors. Related to Figure 2.

(A) Quantitative analysis of relative intensity of p63 staining after 6-day treatment of H9 hESCs using dhS1P (n=1655 cells in 8 images), CYM5542 (n=2229 cells in 9 images), CYM 5520 (n=2360 cells in 9 images), and CYM 5541 (n=2778 cells in 10 images). Data points represent fluorescence intensity in individual cells. Analysis was performed in MATLAB and at least 2 biological replicates were used. (Error bars are S.D.)

(B) Quantitative analysis of cells expressing p63 after 6-day treatment of H9 hESCs using dhS1P (n=1655 cells in 8 images), CYM5542 (n=2229 cells in 9 images), CYM 5520 (n=2360 cells in 9 images), and CYM 5541 (n=2778 cells in 10 images). Data points represent fraction of p63⁺ cells in individual images. Analysis was performed in MATLAB and at least 2 biological replicates were used. (Error bars are S.D.)

(C) Quantitative analysis of relative intensity of p63 staining after 6-day treatment of H1 hESCs using dhS1P (n=2232 cells in 7 images), CYM5542 (n=1471 cells in 5 images), CYM 5520 (n=5768 cells in 17 images), and CYM 5541 (n=26244 in 9 images). Data points represent fluorescence intensity in individual cells. Analysis was performed in MATLAB and at least 2 biological replicates were used. (Error bars are S.D.)

(D) Quantitative analysis of cells expressing p63 of 6-day treatment of H1 hESCs using dhS1P (n=2232 cells in 7 images), CYM5542 (n=1471 cells in 5 images), CYM 5520 (n=5768 cells in 17 images), and CYM 5541 (n=26244 in 9 images). Data points represent fraction of p63⁺ cells in individual images. Analysis was performed in MATLAB and at least 2 biological replicates were used. (Error bars are S.D.)

(E) Quantitative analysis of relative intensity of CDX2 staining after 6-day treatment of H9 hESCs using dhS1P (n=2639 cells in 7 images), CYM5542 (n=1872 cells in 7 images), CYM 5520 (n=4539 cells in 12 images), and CYM 5541 (n=5927 cells in 15 images). Data points represent fluorescence intensity in individual cells. Analysis was performed in MATLAB and at least 2 biological replicates were used. (Error bars are S.D.)

(F) Quantitative analysis of cells expressing CDX2 after 6-day treatment of H9 hESCs using dhS1P (n=2639 cells in 7 images), CYM5542 (n=1872 cells in 7 images), CYM 5520 (n=4539 cells in 12 images), and CYM 5541 (n=5927 cells in 15 images). Data points represent fraction of CDX2⁺ cells in individual images. Analysis was performed in MATLAB and at least 2 biological replicates were used. (Error bars are S.D.)

(G) Quantitative analysis of relative intensity of CDX2 staining after 6-day treatment of H1 hESCs using dhS1P (n=3425 cells in 7 images), CYM5542 (n=4373 cells in 11 images), CYM 5520 (n=3367 cells in 11 images), and CYM 5541 (n=3839 cells in 11 images). Data points represent fluorescence intensity in individual cells. Analysis was performed in MATLAB and at least 2 biological replicates were used. (Error bars are S.D.)

(H) Quantitative analysis of cells expressing CDX2 of 6-day treatment of H1 hESCs using dhS1P (n=3425 cells in 7 images), CYM5542 (n=4373 cells in 11 images), CYM 5520 (n=3367 cells in 11 images), and CYM 5541 (n=3839 cells in 11 images). Data points represent fraction of

CDX2⁺ cells in individual images. Analysis was performed in MATLAB and at least 2 biological replicates were used. (Error bars are S.D., n represents an individual image).

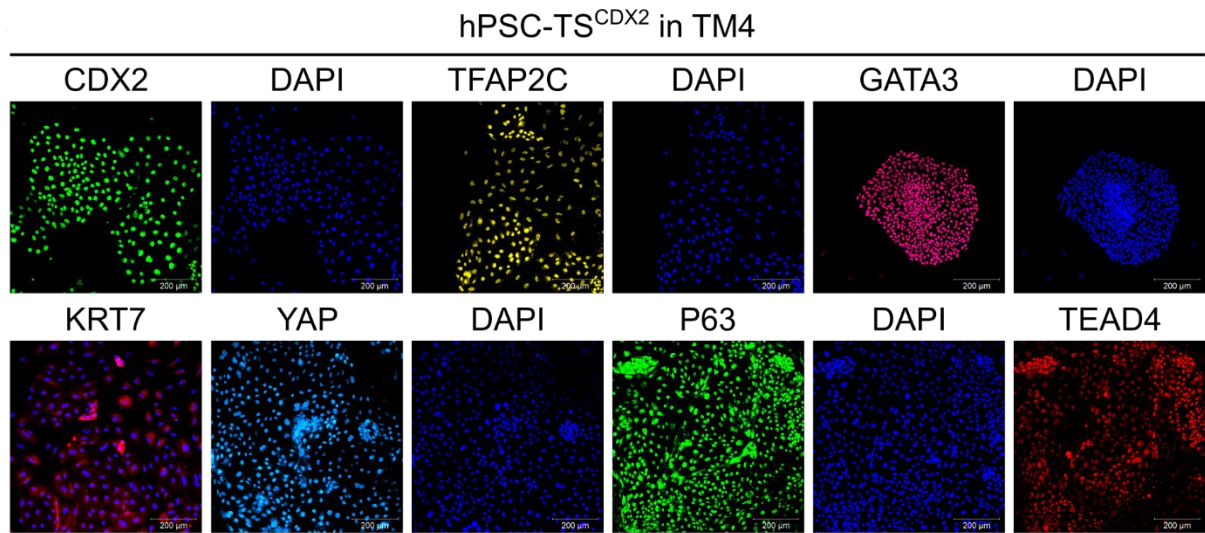


Figure S6: Optimizing timing of hESC differentiation enables derivation of hPSC-TS^{CDX2} cells. Related to Figure 3.

(A) Confocal images of H1 hPSC-TS^{CDX2} in TM4, staining for CDX2, TFAP2C and GATA3, YAP, TEAD4, and P63. Nuclei were stained with DAPI. Scale bars are 200 μm.

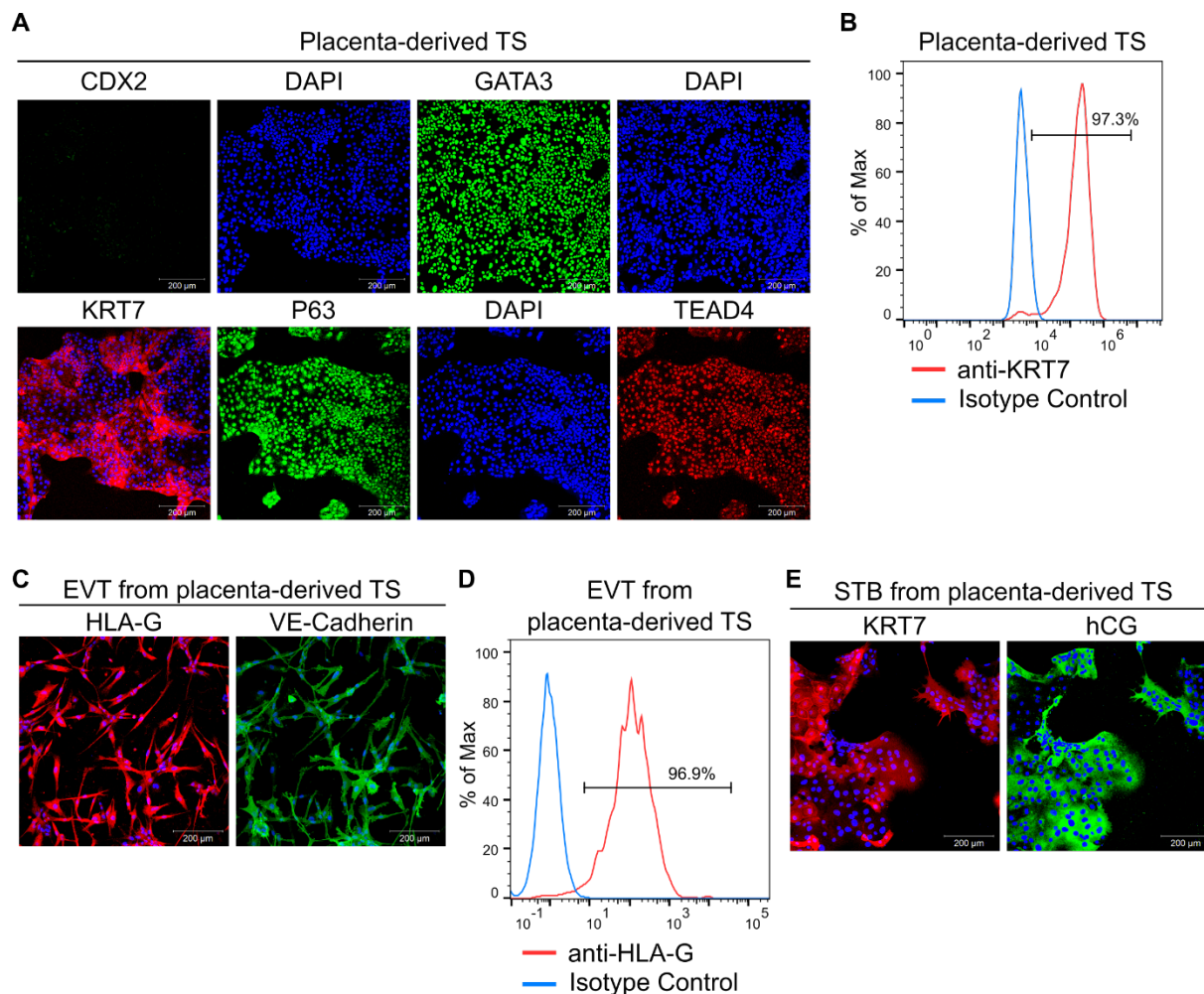


Figure S7: Placenta-derived TS cells. Related to Figure 4.

(A) Confocal images of primary-derived TS cells in TSCM, staining for CDX2, GATA3, TEAD4, and P63. Nuclei were stained with DAPI. Similar results were obtained with another placenta-derived TS cell line. Scale bars.

(B) Flow cytometry histogram of KRT7 expression of primary-derived TS cells compared to isotype control. Similar results were obtained with another placenta-derived TS cell line.

(C) Confocal images of EVTs from primary-derived TS cells, staining for HLA-G and VE-Cadherin. Nuclei were stained with DAPI. Similar results were obtained with another placenta-derived TS cell line. Scale bars are 200µm.

(D) Flow cytometry histogram of HLA-G expression of EVTs from primary-derived TS cells compared to isotype control. Similar results were obtained with another placenta-derived TS cell line.

(E) Confocal images of STB from primary-derived TS cells, staining for KRT7 and hCG. Nuclei were stained with DAPI. Similar results were obtained with another placenta-derived TS cell line. Scale bars are 200µm.

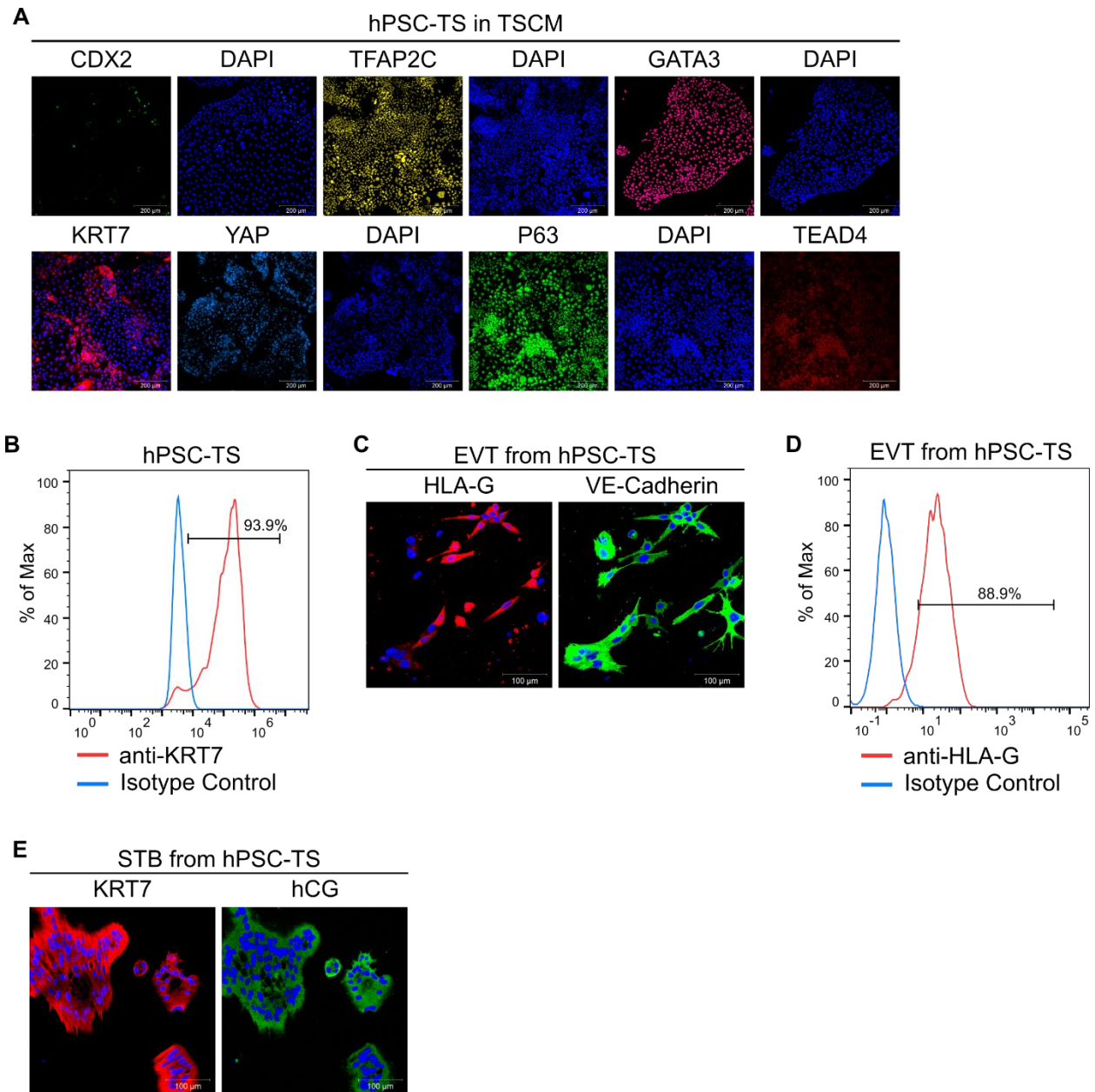


Figure S8: Formation of hPSC-TS cells. Related to Figure 4.

(A) Confocal images of H1 hPSC-TS in TSCM, staining for CDX2, TFAP2C and GATA3, YAP, TEAD4, and P63. Nuclei were stained with DAPI. Scale bars are 200 μm .

(B) Flow cytometry histogram of KRT7 expression of H1 hPSC-TS cells in TSCM compared to isotype control.

(C) Confocal images of EVTs from H1 hPSC-TS cells, staining for HLA-G and VE-Cadherin. Nuclei were stained with DAPI. Scale bars are 100 μm .

(D) Flow cytometry histogram of HLA-G expression of EVTs from H1 hPSC-TS cells compared to isotype control.

(E) Confocal images of STB from H1 hPSC-TS cells, staining for hCG and KRT7. Nuclei were stained with DAPI. Scale bars are 100 μ m.

Methods S1: List of primers used for quantitative PCR analysis

Gene	Primer	Sequence
CDX2	Forward	GGC AGC CAA GTG AAA ACC AG
CDX2	Reverse	GGT GAT GTA GCG ACT GTA GTG AA
CGB	Forward	CAG CAT CCT ATC ACC TCC TGG T
CGB	Reverse	CTG GAA CAT CTC CAT CCT TGG T
CSH1/2	Forward	CAT GAC TCC CAG ACC TCC TTC T
CSH1/2	Reverse	ATT TCT GTT GCG TTT CCT CCA T
ELF5	Forward	GCT GCG ACC AGT ACA AGT TG
ELF5	Reverse	CTG CCT CGA CGA ACT CCT C
GAPDH	Forward	CTC CAC GAC GTA CTC AGC G
GAPDH	Reverse	TGT TGC CAT CAA TGA CCC CTT
HLA-G	Forward	CCA CCA CCC TGT CTT TGA CTA T
HLA-G	Reverse	ACG TCC TGG GTC TGG TCC T
KDR	Forward	GGC CCA ATA ATC AGA GTG GCA
KDR	Reverse	CCA GTG TCA TTT CCG ATC ACT TT
LMO2	Forward	GGC CAT CGA AAG GAA GAG CC
LMO2	Reverse	GGC CCA GTT TGT AGT AGA GGC
MMP2	Forward	TGG CAC CCA TTT ACA CCT ACA C
MMP2	Reverse	ATG TCA GGA GAG GCC CCA TAG A
MSI1	Forward	TAA AGT GCT GGC GCA ATC G
MSI1	Reverse	TCT TCT TCG TTC GAG TCA CCA
NES	Forward	CTG CTA CCC TTG AGA CAC CTG
NES	Reverse	GGG CTC TGA TCT CTG CAT CTA C
OLIG3	Forward	AGC CGT CTC AAC TCG GTC T
OLIG3	Reverse	CAT GGC TAG GTT CAG GTC GTG
SDC1	Forward	CTA TTC CCA CGT CTC CAG AAC C
SDC1	Reverse	GGA CTA CAG CCT CTC CCT CCT T
T	Forward	CTG GGT ACT CCC AAT GGG G
T	Reverse	GGT TGG AGA ATT GTT CCG ATG A
TBX4	Forward	TGT TCC CCA GCT ACA AGG TAA
TBX4	Reverse	GCA GGG ACA ATG TCA ATC AGC
TEAD4	Forward	CAG GTG GTG GAG AAA GTT GAG A
TEAD4	Reverse	GTG CTT GAG CTT GTG GAT GAA G
TP63	Forward	AGA AAC GAA GAT CCC CAG ATG A
TP63	Reverse	CTG TTG CTG TTG CCT GTA CGT T

Supplemental Table S1. Genes identified with significantly higher expression levels in differentiated vs. undifferentiated hESCs. A total of 291 genes are listed here that show a false discovery rate (FDR) q-value<0.05 (based on ANOVA p-values) and fold change (FC) ≥ 1.5 (calculated as the ratio of the average across all differentiated hESC samples over the average across all undifferentiated hESC samples).

EnsembleID	GeneSymbol	p-value	FDR q-value	FC (differentiated hESCs / undifferentiated hESCs)
ENSG00000137203	<i>TFAP2A</i>	5.01E-18	2.04E-14	2.61
ENSG00000006377	<i>DLX6</i>	1.04E-16	1.93E-13	2.56
ENSG00000115596	<i>WNT6</i>	1.29E-16	1.93E-13	2.85
ENSG00000189120	<i>SP6</i>	1.53E-16	1.93E-13	1.51
ENSG00000116729	<i>WLS</i>	2.76E-16	2.99E-13	1.91
ENSG00000115361	<i>ACADL</i>	4.43E-16	4.19E-13	2.25
ENSG00000105880	<i>DLX5</i>	5.91E-16	4.98E-13	2.71
ENSG00000137962	<i>ARHGAP29</i>	7.18E-16	5.44E-13	1.60
ENSG00000064195	<i>DLX3</i>	7.96E-16	5.48E-13	2.02
ENSG00000229950	<i>TFAP2A-AS1</i>	1.70E-15	8.59E-13	1.89
ENSG00000138792	<i>ENPEP</i>	2.41E-15	1.14E-12	2.50
ENSG00000120149	<i>MSX2</i>	2.88E-15	1.28E-12	2.44
ENSG00000144355	<i>DLX1</i>	9.95E-15	3.59E-12	2.65
ENSG00000197308	<i>GATA3-AS1</i>	1.21E-14	4.16E-12	2.38
ENSG00000231764	<i>DLX6-AS1</i>	1.44E-14	4.55E-12	2.47
ENSG00000271824	<i>SMIM32</i>	1.83E-14	5.54E-12	1.97
ENSG00000186212	<i>SOWAHB</i>	2.01E-14	5.71E-12	1.51
ENSG00000075461	<i>CACNG4</i>	2.33E-14	6.32E-12	1.63
ENSG00000115844	<i>DLX2</i>	2.77E-14	7.23E-12	2.64
ENSG00000113196	<i>HAND1</i>	3.19E-14	7.55E-12	3.32
ENSG00000172201	<i>ID4</i>	3.32E-14	7.63E-12	1.71
ENSG00000163132	<i>MSX1</i>	4.34E-14	9.39E-12	2.50
ENSG00000169242	<i>EFNA1</i>	8.38E-14	1.67E-11	1.60
ENSG00000218416	<i>AC110619.1</i>	8.18E-14	1.67E-11	1.88
ENSG00000164741	<i>DLC1</i>	1.47E-13	2.72E-11	1.72
ENSG00000120693	<i>SMAD9</i>	2.19E-13	3.60E-11	1.75
ENSG00000183779	<i>ZNF703</i>	3.96E-13	5.65E-11	1.51
ENSG00000147041	<i>SYTL5</i>	4.17E-13	5.85E-11	2.24
ENSG00000127863	<i>TNFRSF19</i>	5.48E-13	6.80E-11	1.89
ENSG00000163453	<i>IGFBP7</i>	7.31E-13	8.94E-11	1.87
ENSG00000110375	<i>UPK2</i>	1.24E-12	1.28E-10	1.73
ENSG00000108932	<i>SLC16A6</i>	1.28E-12	1.31E-10	2.14
ENSG00000165556	<i>CDX2</i>	1.41E-12	1.42E-10	2.68
ENSG00000154274	<i>C4orf19</i>	3.07E-12	2.67E-10	1.73
ENSG00000140470	<i>ADAMTS17</i>	3.15E-12	2.71E-10	1.85
ENSG00000166450	<i>PRTG</i>	3.48E-12	2.90E-10	1.88
ENSG00000205336	<i>ADGRG1</i>	4.38E-12	3.34E-10	1.88
ENSG00000132170	<i>PPARG</i>	6.40E-12	4.36E-10	2.29
ENSG00000139515	<i>PDX1</i>	6.45E-12	4.36E-10	1.51
ENSG00000112782	<i>CLIC5</i>	1.06E-11	6.54E-10	1.79
ENSG00000170689	<i>HOXB9</i>	1.07E-11	6.54E-10	2.14
ENSG00000118526	<i>TCF21</i>	1.34E-11	7.36E-10	1.79
ENSG00000152315	<i>KCNK13</i>	1.36E-11	7.36E-10	2.04
ENSG00000181634	<i>TNFSF15</i>	1.47E-11	7.50E-10	2.52

ENSG00000183722	<i>LHFPL6</i>	1.70E-11	8.20E-10	1.78
ENSG00000165125	<i>TRPV6</i>	1.72E-11	8.22E-10	1.65
ENSG00000232638	<i>AL390294.1</i>	1.73E-11	8.22E-10	1.65
ENSG00000125637	<i>PSD4</i>	1.76E-11	8.29E-10	1.82
ENSG00000145246	<i>ATP10D</i>	1.91E-11	8.81E-10	1.52
ENSG00000016082	<i>ISL1</i>	1.99E-11	9.14E-10	2.62
ENSG00000249641	<i>HOXC13-AS</i>	2.29E-11	9.89E-10	2.46
ENSG00000275880	<i>ALI39385.1</i>	2.80E-11	1.14E-09	1.57
ENSG00000228412	<i>AL022068.1</i>	2.95E-11	1.18E-09	1.62
ENSG00000198691	<i>ABCA4</i>	3.11E-11	1.23E-09	1.71
ENSG00000168453	<i>HR</i>	3.19E-11	1.24E-09	1.61
ENSG00000197406	<i>DIO3</i>	3.24E-11	1.25E-09	2.23
ENSG00000139055	<i>ERP27</i>	3.66E-11	1.36E-09	2.26
ENSG00000250305	<i>TRMT9B</i>	3.72E-11	1.37E-09	1.53
ENSG00000107485	<i>GATA3</i>	4.08E-11	1.45E-09	2.19
ENSG00000108244	<i>KRT23</i>	5.33E-11	1.68E-09	2.18
ENSG00000120217	<i>CD274</i>	5.23E-11	1.68E-09	1.66
ENSG00000158055	<i>GRHL3</i>	5.16E-11	1.68E-09	1.83
ENSG00000176170	<i>SPHK1</i>	5.11E-11	1.68E-09	1.73
ENSG00000187634	<i>SAMD11</i>	7.23E-11	2.10E-09	1.65
ENSG00000214822	<i>KRT16P3</i>	7.30E-11	2.11E-09	1.93
ENSG00000280623	<i>PCAT14</i>	7.36E-11	2.12E-09	1.87
ENSG00000203805	<i>PLPP4</i>	7.66E-11	2.18E-09	1.79
ENSG00000165566	<i>AMER2</i>	9.40E-11	2.48E-09	2.17
ENSG00000111186	<i>WNT5B</i>	9.75E-11	2.54E-09	1.52
ENSG00000150556	<i>LYPD6B</i>	9.79E-11	2.54E-09	1.67
ENSG00000164850	<i>GPER1</i>	1.22E-10	2.94E-09	1.53
ENSG00000060718	<i>COL11A1</i>	1.33E-10	3.13E-09	1.54
ENSG00000144476	<i>ACKR3</i>	1.38E-10	3.22E-09	2.15
ENSG00000102445	<i>RUBCNL</i>	1.53E-10	3.43E-09	1.65
ENSG00000178695	<i>KCTD12</i>	1.84E-10	3.98E-09	1.53
ENSG00000139793	<i>MBNL2</i>	1.97E-10	4.21E-09	1.88
ENSG00000186594	<i>MIR22HG</i>	2.23E-10	4.60E-09	1.57
ENSG00000123364	<i>HOXC13</i>	2.26E-10	4.64E-09	2.47
ENSG00000183018	<i>SPNS2</i>	2.36E-10	4.72E-09	1.89
ENSG00000251538	<i>LINC02201</i>	2.44E-10	4.85E-09	1.56
ENSG00000005108	<i>THSD7A</i>	2.54E-10	5.03E-09	1.53
ENSG00000198223	<i>CSF2RA</i>	2.58E-10	5.09E-09	1.73
ENSG00000184304	<i>PRKD1</i>	2.66E-10	5.17E-09	1.64
ENSG00000142700	<i>DMRTA2</i>	2.94E-10	5.62E-09	2.30
ENSG00000125945	<i>ZNF436</i>	3.01E-10	5.69E-09	1.58
ENSG00000138119	<i>MYOF</i>	3.15E-10	5.89E-09	2.02
ENSG00000138061	<i>CYP11B1</i>	3.45E-10	6.31E-09	1.52
ENSG00000113494	<i>PRLR</i>	3.47E-10	6.33E-09	1.66
ENSG00000139144	<i>PIK3C2G</i>	3.95E-10	6.90E-09	1.79
ENSG00000198944	<i>SOWAHA</i>	4.45E-10	7.62E-09	1.92
ENSG00000070731	<i>ST6GALNAC2</i>	4.48E-10	7.64E-09	1.51
ENSG00000179348	<i>GATA2</i>	4.58E-10	7.75E-09	1.72
ENSG00000164778	<i>EN2</i>	5.01E-10	8.30E-09	2.42
ENSG00000144619	<i>CNTN4</i>	5.26E-10	8.55E-09	1.86
ENSG00000076356	<i>PLXNA2</i>	5.41E-10	8.72E-09	1.66
ENSG00000115594	<i>IL1R1</i>	5.81E-10	9.29E-09	1.64

ENSG00000227121	<i>AC073174.1</i>	5.81E-10	9.29E-09	1.68
ENSG00000135111	<i>TBX3</i>	5.82E-10	9.29E-09	2.15
ENSG00000138449	<i>SLC40A1</i>	6.36E-10	9.87E-09	1.67
ENSG00000145721	<i>LIX1</i>	6.39E-10	9.88E-09	2.44
ENSG00000184292	<i>TACSTD2</i>	7.90E-10	1.15E-08	1.72
ENSG00000278952	<i>AP003068.4</i>	9.52E-10	1.30E-08	1.56
ENSG00000150687	<i>PRSS23</i>	9.69E-10	1.31E-08	1.58
ENSG00000143217	<i>NECTIN4</i>	1.04E-09	1.38E-08	1.72
ENSG00000166401	<i>SERPINB8</i>	1.11E-09	1.43E-08	1.63
ENSG00000164619	<i>BMPER</i>	1.11E-09	1.44E-08	1.67
ENSG00000170379	<i>TCAF2</i>	1.15E-09	1.48E-08	1.71
ENSG00000148677	<i>ANKRD1</i>	1.19E-09	1.52E-08	2.53
ENSG00000166963	<i>MAP1A</i>	1.34E-09	1.64E-08	1.60
ENSG00000172296	<i>SPTLC3</i>	1.35E-09	1.65E-08	1.87
ENSG00000143248	<i>RGS5</i>	1.38E-09	1.67E-08	1.60
ENSG00000244300	<i>GATA2-AS1</i>	1.64E-09	1.90E-08	1.94
ENSG00000109436	<i>TBC1D9</i>	1.65E-09	1.91E-08	1.82
ENSG00000141579	<i>ZNF750</i>	1.91E-09	2.10E-08	1.66
ENSG00000064655	<i>EYA2</i>	2.14E-09	2.25E-08	1.64
ENSG00000236651	<i>DLX2-AS1</i>	2.33E-09	2.39E-08	1.51
ENSG00000198774	<i>RASSF9</i>	2.79E-09	2.73E-08	1.89
ENSG00000138795	<i>LEF1</i>	2.83E-09	2.75E-08	1.63
ENSG00000206384	<i>COL6A6</i>	2.83E-09	2.75E-08	1.73
ENSG00000118777	<i>ABCG2</i>	2.91E-09	2.79E-08	1.87
ENSG00000081479	<i>LRP2</i>	3.00E-09	2.86E-08	1.61
ENSG00000164604	<i>GPR85</i>	3.00E-09	2.86E-08	1.54
ENSG00000259977	<i>ALI21578.3</i>	3.06E-09	2.90E-08	1.79
ENSG00000120937	<i>NPPB</i>	3.08E-09	2.91E-08	2.23
ENSG00000260034	<i>LCMT1-AS2</i>	3.22E-09	3.02E-08	1.82
ENSG00000182118	<i>FAM89A</i>	3.54E-09	3.24E-08	1.71
ENSG00000182752	<i>PAPPA</i>	3.73E-09	3.36E-08	1.58
ENSG00000145681	<i>HAPLN1</i>	3.81E-09	3.42E-08	1.73
ENSG00000108576	<i>SLC6A4</i>	3.84E-09	3.43E-08	1.55
ENSG00000008196	<i>TFAP2B</i>	4.17E-09	3.67E-08	2.28
ENSG00000259663	<i>AC010478.1</i>	4.18E-09	3.67E-08	2.05
ENSG00000181291	<i>TMEM132E</i>	5.43E-09	4.47E-08	1.70
ENSG00000258498	<i>DIO3OS</i>	5.47E-09	4.49E-08	2.31
ENSG00000047365	<i>ARAP2</i>	6.39E-09	5.07E-08	1.54
ENSG00000277228	<i>ALI38686.1</i>	6.49E-09	5.14E-08	1.87
ENSG00000162552	<i>WNT4</i>	6.87E-09	5.34E-08	1.75
ENSG00000211448	<i>DIO2</i>	7.62E-09	5.78E-08	1.83
ENSG00000264230	<i>ANXA8L1</i>	8.86E-09	6.41E-08	1.84
ENSG00000250303	<i>AP002884.1</i>	8.91E-09	6.44E-08	1.62
ENSG00000040731	<i>CDH10</i>	9.44E-09	6.72E-08	2.05
ENSG00000176907	<i>TCIM</i>	9.52E-09	6.76E-08	2.66
ENSG00000170801	<i>HTRA3</i>	9.78E-09	6.91E-08	1.58
ENSG00000133519	<i>ZDHHC8P1</i>	9.95E-09	7.00E-08	1.56
ENSG00000135046	<i>ANXA1</i>	1.03E-08	7.24E-08	2.13
ENSG00000122012	<i>SV2C</i>	1.07E-08	7.45E-08	1.56
ENSG00000163803	<i>PLB1</i>	1.20E-08	8.06E-08	1.57
ENSG00000222014	<i>RAB6C</i>	1.23E-08	8.23E-08	1.70
ENSG00000115474	<i>KCNJ13</i>	1.37E-08	8.92E-08	1.90

ENSG00000108511	<i>HOXB6</i>	1.42E-08	9.14E-08	2.64
ENSG00000265246	<i>ACI29926.1</i>	1.42E-08	9.16E-08	1.52
ENSG00000166741	<i>NNMT</i>	1.60E-08	1.00E-07	1.72
ENSG00000180875	<i>GREM2</i>	1.66E-08	1.03E-07	1.55
ENSG00000162931	<i>TRIM17</i>	1.71E-08	1.05E-07	1.56
ENSG00000156466	<i>GDF6</i>	1.72E-08	1.05E-07	2.51
ENSG00000137440	<i>FGFBP1</i>	1.78E-08	1.08E-07	1.59
ENSG00000092295	<i>TGM1</i>	1.83E-08	1.10E-07	1.54
ENSG00000174640	<i>SLCO2A1</i>	1.86E-08	1.12E-07	1.75
ENSG00000158955	<i>WNT9B</i>	1.88E-08	1.12E-07	2.17
ENSG00000147883	<i>CDKN2B</i>	1.95E-08	1.15E-07	2.01
ENSG00000147408	<i>CSGALNACT1</i>	2.33E-08	1.31E-07	1.93
ENSG00000167767	<i>KRT80</i>	2.86E-08	1.55E-07	2.00
ENSG00000140873	<i>ADAMTS18</i>	3.25E-08	1.70E-07	2.04
ENSG00000169129	<i>AFAP1L2</i>	3.55E-08	1.81E-07	1.60
ENSG00000125398	<i>SOX9</i>	3.77E-08	1.90E-07	1.53
ENSG00000159216	<i>RUNX1</i>	3.77E-08	1.90E-07	1.58
ENSG00000251348	<i>HSPD1P11</i>	3.94E-08	1.96E-07	1.51
ENSG00000143995	<i>MEIS1</i>	4.52E-08	2.17E-07	2.46
ENSG00000158270	<i>COLEC12</i>	6.91E-08	2.99E-07	1.59
ENSG00000105251	<i>SHD</i>	8.26E-08	3.44E-07	1.64
ENSG00000041982	<i>TNC</i>	8.67E-08	3.57E-07	1.89
ENSG00000144227	<i>NXPH2</i>	9.72E-08	3.89E-07	1.63
ENSG00000246273	<i>SBF2-AS1</i>	9.92E-08	3.93E-07	1.51
ENSG00000215612	<i>HMX1</i>	1.01E-07	3.98E-07	1.83
ENSG00000276850	<i>AC245041.2</i>	1.04E-07	4.07E-07	1.52
ENSG00000183691	<i>NOG</i>	1.06E-07	4.14E-07	2.10
ENSG00000172548	<i>NIPAL4</i>	1.15E-07	4.44E-07	1.91
ENSG00000170396	<i>ZNF804A</i>	1.22E-07	4.64E-07	1.60
ENSG00000170807	<i>LMOD2</i>	1.22E-07	4.65E-07	1.55
ENSG00000185551	<i>NR2F2</i>	1.22E-07	4.65E-07	2.02
ENSG00000169554	<i>ZEB2</i>	1.32E-07	4.94E-07	1.69
ENSG00000118729	<i>CASQ2</i>	1.35E-07	5.02E-07	2.07
ENSG00000069011	<i>PITX1</i>	1.41E-07	5.21E-07	1.69
ENSG00000102683	<i>SGCG</i>	1.57E-07	5.66E-07	1.62
ENSG00000110195	<i>FOLR1</i>	1.73E-07	6.12E-07	1.59
ENSG00000102243	<i>VGLL1</i>	1.81E-07	6.34E-07	1.91
ENSG00000259727	<i>AC103740.2</i>	1.83E-07	6.39E-07	1.76
ENSG00000116016	<i>EPAS1</i>	1.98E-07	6.81E-07	1.73
ENSG00000169247	<i>SH3TC2</i>	2.06E-07	7.00E-07	1.52
ENSG00000273472	<i>AC096733.2</i>	2.09E-07	7.07E-07	1.82
ENSG00000149090	<i>PAMR1</i>	2.23E-07	7.40E-07	1.53
ENSG00000158014	<i>SLC30A2</i>	2.32E-07	7.61E-07	1.67
ENSG00000082293	<i>COL19A1</i>	2.37E-07	7.75E-07	1.98
ENSG00000198842	<i>DUSP27</i>	2.59E-07	8.30E-07	1.60
ENSG00000140795	<i>MYLK3</i>	2.72E-07	8.66E-07	1.54
ENSG00000122691	<i>TWIST1</i>	3.06E-07	9.43E-07	1.83
ENSG00000013588	<i>GPRC5A</i>	3.20E-07	9.76E-07	1.62
ENSG00000183023	<i>SLC8A1</i>	3.82E-07	1.13E-06	1.87
ENSG00000183801	<i>OLFML1</i>	4.12E-07	1.19E-06	1.82
ENSG00000171056	<i>SOX7</i>	4.18E-07	1.20E-06	1.80
ENSG00000119242	<i>CCDC92</i>	4.35E-07	1.24E-06	1.72

ENSG00000163823	<i>CCR1</i>	4.38E-07	1.25E-06	1.87
ENSG00000182168	<i>UNC5C</i>	4.51E-07	1.28E-06	1.98
ENSG00000169550	<i>MUC15</i>	4.60E-07	1.30E-06	1.56
ENSG00000231817	<i>LINC01198</i>	4.61E-07	1.30E-06	1.93
ENSG00000175591	<i>P2RY2</i>	5.02E-07	1.39E-06	1.71
ENSG00000073282	<i>TP63</i>	5.50E-07	1.49E-06	2.18
ENSG00000248409	<i>AP000344.2</i>	5.77E-07	1.55E-06	1.53
ENSG00000133110	<i>POSTN</i>	6.32E-07	1.67E-06	1.59
ENSG00000137872	<i>SEMA6D</i>	6.60E-07	1.73E-06	1.69
ENSG00000143867	<i>OSR1</i>	6.68E-07	1.74E-06	1.69
ENSG00000155622	<i>XAGE2</i>	7.83E-07	1.98E-06	1.52
ENSG00000061455	<i>PRDM6</i>	8.44E-07	2.10E-06	1.58
ENSG00000260027	<i>HOXB7</i>	8.74E-07	2.16E-06	1.72
ENSG00000111348	<i>ARHGDIB</i>	8.85E-07	2.18E-06	1.73
ENSG00000150551	<i>LYPD1</i>	9.49E-07	2.31E-06	1.51
ENSG00000014257	<i>ACPP</i>	9.67E-07	2.35E-06	1.52
ENSG00000168702	<i>LRP1B</i>	1.05E-06	2.50E-06	1.82
ENSG00000132746	<i>ALDH3B2</i>	1.13E-06	2.66E-06	1.56
ENSG00000101846	<i>STS</i>	1.20E-06	2.79E-06	1.63
ENSG00000186369	<i>LINC00643</i>	1.25E-06	2.87E-06	2.00
ENSG00000138271	<i>GPR87</i>	1.31E-06	2.98E-06	1.66
ENSG00000141052	<i>MYOCD</i>	1.38E-06	3.11E-06	1.56
ENSG00000152229	<i>PSTPIP2</i>	1.65E-06	3.59E-06	1.63
ENSG00000137747	<i>TMPRSS13</i>	1.71E-06	3.70E-06	1.59
ENSG00000042980	<i>ADAM28</i>	1.73E-06	3.75E-06	1.64
ENSG00000128422	<i>KRT17</i>	1.88E-06	3.99E-06	1.65
ENSG00000164683	<i>HEY1</i>	1.89E-06	4.02E-06	1.53
ENSG00000150782	<i>IL18</i>	1.89E-06	4.02E-06	1.62
ENSG00000134138	<i>MEIS2</i>	2.49E-06	5.03E-06	2.02
ENSG00000155011	<i>DKK2</i>	2.79E-06	5.53E-06	1.56
ENSG00000160886	<i>LY6K</i>	2.85E-06	5.61E-06	1.55
ENSG00000165124	<i>SVEP1</i>	2.86E-06	5.62E-06	1.53
ENSG00000253308	<i>AC004080.1</i>	3.36E-06	6.42E-06	1.59
ENSG00000146674	<i>IGFBP3</i>	3.45E-06	6.57E-06	1.92
ENSG00000106038	<i>EVX1</i>	3.82E-06	7.18E-06	1.97
ENSG00000183729	<i>NPBWR1</i>	3.90E-06	7.29E-06	1.76
ENSG00000159251	<i>ACTC1</i>	4.09E-06	7.56E-06	1.79
ENSG00000134258	<i>VTCN1</i>	4.37E-06	7.98E-06	2.44
ENSG00000126016	<i>AMOT</i>	4.92E-06	8.82E-06	1.54
ENSG00000125848	<i>FLRT3</i>	5.71E-06	9.94E-06	1.95
ENSG00000254202	<i>AC015522.1</i>	6.79E-06	1.15E-05	1.81
ENSG00000271474	<i>AC106881.1</i>	6.83E-06	1.15E-05	1.57
ENSG00000260401	<i>AP002761.4</i>	7.25E-06	1.21E-05	1.72
ENSG00000224940	<i>PRRT4</i>	8.25E-06	1.35E-05	1.79
ENSG00000227019	<i>OR7E101P</i>	8.70E-06	1.41E-05	1.52
ENSG00000149596	<i>JPH2</i>	1.01E-05	1.59E-05	1.62
ENSG00000159176	<i>CSRP1</i>	1.06E-05	1.66E-05	1.58
ENSG00000171631	<i>P2RY6</i>	1.10E-05	1.70E-05	2.12
ENSG00000180999	<i>C1orf105</i>	1.17E-05	1.79E-05	2.19
ENSG00000159248	<i>GJD2</i>	1.18E-05	1.80E-05	1.70
ENSG00000175445	<i>LPL</i>	1.53E-05	2.25E-05	1.61
ENSG00000125089	<i>SH3TC1</i>	1.55E-05	2.27E-05	1.57

ENSG00000170214	<i>ADRA1B</i>	1.61E-05	2.35E-05	1.86
ENSG00000043039	<i>BARX2</i>	1.66E-05	2.41E-05	2.00
ENSG00000141449	<i>GREB1L</i>	1.77E-05	2.54E-05	1.71
ENSG00000227300	<i>KRT16P2</i>	1.89E-05	2.68E-05	1.61
ENSG00000169594	<i>BNC1</i>	1.94E-05	2.75E-05	2.00
ENSG00000196878	<i>LAMB3</i>	2.06E-05	2.90E-05	1.69
ENSG00000164879	<i>CA3</i>	2.65E-05	3.59E-05	1.78
ENSG00000120075	<i>HOXB5</i>	2.67E-05	3.61E-05	1.74
ENSG00000128918	<i>ALDH1A2</i>	2.72E-05	3.67E-05	1.60
ENSG00000157551	<i>KCNJ15</i>	2.76E-05	3.71E-05	1.51
ENSG00000120068	<i>HOXB8</i>	3.27E-05	4.29E-05	1.65
ENSG00000214856	<i>KRT16P1</i>	4.52E-05	5.64E-05	1.69
ENSG00000154342	<i>WNT3A</i>	4.63E-05	5.76E-05	1.57
ENSG00000182742	<i>HOXB4</i>	4.68E-05	5.81E-05	1.62
ENSG00000174099	<i>MSRB3</i>	4.93E-05	6.07E-05	1.50
ENSG00000229557	<i>LINC00379</i>	5.51E-05	6.66E-05	1.76
ENSG00000136167	<i>LCPI</i>	6.20E-05	7.37E-05	1.74
ENSG00000115221	<i>ITGB6</i>	8.72E-05	9.90E-05	1.72
ENSG00000173917	<i>HOXB2</i>	1.16E-04	1.27E-04	1.58
ENSG00000147573	<i>TRIM55</i>	1.43E-04	1.52E-04	1.86
ENSG00000204335	<i>SP5</i>	1.69E-04	1.76E-04	1.56
ENSG00000186832	<i>KRT16</i>	2.02E-04	2.05E-04	1.60
ENSG00000143199	<i>ADCY10</i>	2.16E-04	2.17E-04	1.56
ENSG00000121577	<i>POPDC2</i>	2.27E-04	2.26E-04	1.58
ENSG00000182836	<i>PLCXD3</i>	2.87E-04	2.77E-04	1.67
ENSG00000254293	<i>AC026688.2</i>	3.60E-04	3.36E-04	1.65
ENSG00000168542	<i>COL3A1</i>	3.71E-04	3.45E-04	1.80
ENSG00000019549	<i>SNAI2</i>	3.92E-04	3.62E-04	1.79
ENSG00000120093	<i>HOXB3</i>	3.95E-04	3.64E-04	1.52
ENSG00000132854	<i>KANK4</i>	4.03E-04	3.70E-04	1.68
ENSG00000198959	<i>TGM2</i>	5.02E-04	4.50E-04	1.51
ENSG00000158258	<i>CLSTN2</i>	5.06E-04	4.53E-04	1.52
ENSG00000164116	<i>GUCY1A1</i>	7.61E-04	6.47E-04	1.71
ENSG00000172005	<i>MAL</i>	8.62E-04	7.19E-04	1.62
ENSG00000105492	<i>SIGLEC6</i>	1.22E-03	9.73E-04	1.53
ENSG00000122641	<i>INHBA</i>	1.23E-03	9.81E-04	1.51
ENSG00000205221	<i>VIT</i>	1.39E-03	1.09E-03	1.61
ENSG00000139329	<i>LUM</i>	4.17E-03	2.87E-03	1.90
ENSG00000182578	<i>CSF1R</i>	4.79E-03	3.23E-03	1.55

Supplemental Table S2. Genes identified with significantly lower expression levels in differentiated vs. undifferentiated hESCs. A total of 330 genes are listed here that show a false discovery rate (FDR) q-value<0.05 (based on ANOVA p-values) and fold change (FC) ≥ 1.5 (calculated as the ratio of the average across all differentiated hESC samples over the average across all undifferentiated hESC samples).

EnsembleID	GeneSymbol	p-value	FDR q-value	FC (differentiated hESCs / undifferentiated hESCs)
ENSG00000131187	<i>F12</i>	2.04E-14	5.71E-12	-1.80
ENSG00000090932	<i>DLL3</i>	1.34E-13	2.53E-11	-1.89
ENSG00000197408	<i>CYP2B6</i>	1.62E-12	1.59E-10	-2.01
ENSG00000135324	<i>MRAP2</i>	1.68E-12	1.64E-10	-1.67
ENSG00000163530	<i>DPPA2</i>	4.19E-12	3.31E-10	-1.64
ENSG00000154556	<i>SORBS2</i>	1.18E-11	6.97E-10	-2.15
ENSG00000171885	<i>AQP4</i>	1.28E-11	7.26E-10	-1.69
ENSG00000153902	<i>LGI4</i>	1.48E-11	7.51E-10	-2.06
ENSG00000214922	<i>HLA-F-AS1</i>	1.53E-11	7.66E-10	-1.65
ENSG00000144596	<i>GRIP2</i>	1.68E-11	8.20E-10	-1.68
ENSG00000167617	<i>CDC42EP5</i>	2.11E-11	9.46E-10	-1.70
ENSG00000154027	<i>AK5</i>	2.44E-11	1.03E-09	-1.50
ENSG00000100985	<i>MMP9</i>	2.59E-11	1.07E-09	-1.65
ENSG00000169116	<i>PARM1</i>	3.19E-11	1.24E-09	-1.70
ENSG00000266964	<i>FXYP1</i>	3.28E-11	1.25E-09	-1.92
ENSG00000279619	<i>AC020907.5</i>	3.51E-11	1.31E-09	-2.09
ENSG00000118160	<i>SLC8A2</i>	3.75E-11	1.37E-09	-1.60
ENSG00000260776	<i>AC104758.3</i>	4.96E-11	1.68E-09	-1.75
ENSG00000108387	<i>SEPT4</i>	5.16E-11	1.68E-09	-1.66
ENSG00000132481	<i>TRIM47</i>	5.28E-11	1.68E-09	-1.53
ENSG00000110090	<i>CPT1A</i>	5.48E-11	1.70E-09	-2.07
ENSG00000182389	<i>CACNB4</i>	6.58E-11	1.95E-09	-1.71
ENSG00000185666	<i>SYN3</i>	7.71E-11	2.18E-09	-1.81
ENSG00000104833	<i>TUBB4A</i>	9.50E-11	2.50E-09	-1.88
ENSG00000160161	<i>CILP2</i>	1.26E-10	3.00E-09	-1.53
ENSG00000166897	<i>ELFN2</i>	1.35E-10	3.15E-09	-1.71
ENSG00000135423	<i>GLS2</i>	1.39E-10	3.22E-09	-1.67
ENSG00000186648	<i>CARMIL3</i>	1.43E-10	3.28E-09	-1.51
ENSG00000105639	<i>JAK3</i>	1.48E-10	3.36E-09	-1.54
ENSG00000254339	<i>AC064802.1</i>	1.62E-10	3.59E-09	-2.54
ENSG00000182379	<i>NXPH4</i>	1.71E-10	3.76E-09	-1.56
ENSG00000126583	<i>PRKCG</i>	1.76E-10	3.84E-09	-1.51
ENSG00000237886	<i>NALTI</i>	1.77E-10	3.87E-09	-1.51
ENSG0000026950	<i>BTN3A1</i>	1.98E-10	4.21E-09	-1.62
ENSG00000250328	<i>AC022101.1</i>	2.04E-10	4.33E-09	-1.67
ENSG00000155886	<i>SLC24A2</i>	2.08E-10	4.37E-09	-2.09
ENSG00000186470	<i>BTN3A2</i>	2.24E-10	4.62E-09	-1.66
ENSG00000163053	<i>SLC16A14</i>	2.92E-10	5.59E-09	-1.56
ENSG00000117322	<i>CR2</i>	2.98E-10	5.65E-09	-1.61
ENSG00000105376	<i>ICAM5</i>	3.36E-10	6.20E-09	-1.72
ENSG00000169760	<i>NLGN1</i>	3.54E-10	6.40E-09	-1.55
ENSG00000129991	<i>TNNI3</i>	3.76E-10	6.70E-09	-1.98
ENSG00000174950	<i>CD164L2</i>	3.84E-10	6.78E-09	-1.52
ENSG00000159289	<i>GOLGA6A</i>	4.88E-10	8.15E-09	-1.66

ENSG00000138316	<i>ADAMTS14</i>	5.00E-10	8.30E-09	-1.57
ENSG00000148408	<i>CACNA1B</i>	5.06E-10	8.37E-09	-1.60
ENSG00000196132	<i>MYT1</i>	5.97E-10	9.43E-09	-1.68
ENSG00000173258	<i>ZNF483</i>	6.49E-10	9.98E-09	-1.52
ENSG00000182866	<i>LCK</i>	6.74E-10	1.02E-08	-2.16
ENSG00000102096	<i>PIM2</i>	6.79E-10	1.03E-08	-1.51
ENSG00000101336	<i>HCK</i>	6.88E-10	1.03E-08	-1.51
ENSG00000101276	<i>SLC52A3</i>	6.96E-10	1.04E-08	-1.66
ENSG00000144583	<i>MARCH4</i>	7.40E-10	1.09E-08	-1.52
ENSG00000075388	<i>FGF4</i>	7.69E-10	1.12E-08	-2.00
ENSG00000089847	<i>ANKRD24</i>	7.66E-10	1.12E-08	-1.51
ENSG00000103184	<i>SEC14L5</i>	7.68E-10	1.12E-08	-1.64
ENSG00000221946	<i>FXYP7</i>	8.66E-10	1.23E-08	-1.86
ENSG00000132622	<i>HSPA12B</i>	9.33E-10	1.28E-08	-1.71
ENSG00000167994	<i>RAB31L1</i>	9.63E-10	1.31E-08	-1.53
ENSG00000229191	<i>AL358473.1</i>	9.81E-10	1.32E-08	-1.77
ENSG00000103253	<i>HAGHL</i>	9.84E-10	1.32E-08	-1.53
ENSG00000068831	<i>RASGRP2</i>	1.07E-09	1.40E-08	-1.89
ENSG00000159733	<i>ZFYVE28</i>	1.27E-09	1.58E-08	-1.58
ENSG00000152578	<i>GRIA4</i>	1.31E-09	1.61E-08	-2.09
ENSG00000135298	<i>ADGRB3</i>	1.40E-09	1.69E-08	-1.69
ENSG00000101695	<i>RNF125</i>	1.41E-09	1.69E-08	-1.71
ENSG00000228624	<i>HDAC2-AS2</i>	1.44E-09	1.72E-08	-1.65
ENSG00000214944	<i>ARHGEF28</i>	1.72E-09	1.96E-08	-1.50
ENSG00000126733	<i>DACH2</i>	1.72E-09	1.96E-08	-1.54
ENSG00000186340	<i>THBS2</i>	1.80E-09	2.01E-08	-1.88
ENSG00000237923	<i>LINC02570</i>	1.83E-09	2.03E-08	-1.78
ENSG00000141506	<i>PIK3R5</i>	1.95E-09	2.12E-08	-1.65
ENSG00000133101	<i>CCNA1</i>	1.99E-09	2.17E-08	-1.69
ENSG00000112494	<i>UNC93A</i>	2.08E-09	2.22E-08	-1.55
ENSG00000169220	<i>RGS14</i>	2.11E-09	2.24E-08	-1.54
ENSG00000176654	<i>NANOGP1</i>	2.12E-09	2.24E-08	-1.96
ENSG00000160471	<i>COX6B2</i>	2.15E-09	2.26E-08	-1.56
ENSG00000214076	<i>CPSF1P1</i>	2.22E-09	2.32E-08	-1.86
ENSG00000105409	<i>ATPIA3</i>	2.51E-09	2.54E-08	-1.95
ENSG00000198547	<i>C20orf203</i>	2.63E-09	2.62E-08	-1.61
ENSG00000137463	<i>MGARP</i>	2.66E-09	2.64E-08	-1.64
ENSG00000127418	<i>FGFRL1</i>	2.77E-09	2.72E-08	-1.50
ENSG00000167619	<i>TMEM145</i>	2.78E-09	2.72E-08	-1.55
ENSG00000172350	<i>ABCG4</i>	2.88E-09	2.77E-08	-1.51
ENSG00000076344	<i>RGS11</i>	2.93E-09	2.82E-08	-1.54
ENSG00000169302	<i>STK32A</i>	3.03E-09	2.88E-08	-1.51
ENSG00000095932	<i>SMIM24</i>	3.24E-09	3.03E-08	-1.67
ENSG00000106633	<i>GCK</i>	3.45E-09	3.19E-08	-1.60
ENSG00000166073	<i>GPR176</i>	3.49E-09	3.21E-08	-1.67
ENSG00000248746	<i>ACTN3</i>	3.83E-09	3.42E-08	-1.70
ENSG00000111344	<i>RASAL1</i>	3.97E-09	3.52E-08	-1.58
ENSG00000111704	<i>NANOG</i>	4.05E-09	3.58E-08	-2.31
ENSG00000117245	<i>KIF17</i>	4.14E-09	3.64E-08	-1.55
ENSG00000129451	<i>KLK10</i>	4.22E-09	3.69E-08	-1.59
ENSG00000167748	<i>KLK1</i>	4.39E-09	3.81E-08	-1.51
ENSG00000159403	<i>CIR</i>	4.48E-09	3.88E-08	-1.57

ENSG00000092051	<i>JPH4</i>	4.81E-09	4.09E-08	-2.12
ENSG00000261949	<i>GFY</i>	4.95E-09	4.20E-08	-1.55
ENSG00000225889	<i>AC012368.1</i>	5.17E-09	4.30E-08	-1.84
ENSG00000160712	<i>IL6R</i>	5.49E-09	4.50E-08	-1.75
ENSG00000054179	<i>ENTPD2</i>	5.59E-09	4.57E-08	-1.61
ENSG00000145794	<i>MEGF10</i>	5.60E-09	4.57E-08	-1.54
ENSG00000176884	<i>GRIN1</i>	5.61E-09	4.58E-08	-1.58
ENSG00000154096	<i>THY1</i>	6.54E-09	5.17E-08	-1.55
ENSG00000130813	<i>CI9orf66</i>	6.68E-09	5.24E-08	-1.62
ENSG00000174482	<i>LINGO2</i>	6.82E-09	5.33E-08	-1.52
ENSG00000206791	<i>RNU1-129P</i>	6.85E-09	5.34E-08	-1.58
ENSG00000183778	<i>B3GALT5</i>	7.20E-09	5.53E-08	-1.59
ENSG00000116852	<i>KIF21B</i>	7.21E-09	5.54E-08	-1.52
ENSG00000236673	<i>AL117378.1</i>	7.49E-09	5.71E-08	-2.26
ENSG00000136267	<i>DGKB</i>	7.58E-09	5.76E-08	-1.69
ENSG00000224945	<i>AL353150.1</i>	7.76E-09	5.86E-08	-1.51
ENSG00000101000	<i>PROCR</i>	7.80E-09	5.87E-08	-1.62
ENSG00000005513	<i>SOX8</i>	8.49E-09	6.22E-08	-1.51
ENSG00000069535	<i>MAOB</i>	8.52E-09	6.23E-08	-1.59
ENSG00000162004	<i>CCDC78</i>	9.17E-09	6.57E-08	-1.66
ENSG00000198576	<i>ARC</i>	9.41E-09	6.71E-08	-1.82
ENSG00000155629	<i>PIK3API</i>	9.42E-09	6.72E-08	-1.65
ENSG00000204642	<i>HLA-F</i>	9.88E-09	6.97E-08	-1.58
ENSG00000002746	<i>HECW1</i>	1.19E-08	8.05E-08	-1.60
ENSG00000136840	<i>ST6GALNAC4</i>	1.23E-08	8.23E-08	-1.53
ENSG00000072657	<i>TRHDE</i>	1.29E-08	8.51E-08	-1.64
ENSG00000142405	<i>NLRP12</i>	1.30E-08	8.54E-08	-1.77
ENSG00000186439	<i>TRDN</i>	1.34E-08	8.75E-08	-1.84
ENSG00000280511	<i>AL591030.1</i>	1.34E-08	8.75E-08	-1.66
ENSG00000068976	<i>PYGM</i>	1.40E-08	9.07E-08	-1.50
ENSG00000189292	<i>ALKAL2</i>	1.48E-08	9.47E-08	-1.51
ENSG00000149926	<i>FAM57B</i>	1.54E-08	9.76E-08	-1.75
ENSG00000158825	<i>CDA</i>	1.56E-08	9.87E-08	-1.65
ENSG00000186297	<i>GABRA5</i>	1.57E-08	9.90E-08	-1.52
ENSG00000183971	<i>NPW</i>	1.70E-08	1.05E-07	-1.56
ENSG00000074317	<i>SNCB</i>	1.75E-08	1.07E-07	-1.65
ENSG00000105642	<i>KCNN1</i>	1.85E-08	1.11E-07	-1.53
ENSG00000185386	<i>MAPK11</i>	1.90E-08	1.13E-07	-1.55
ENSG00000145536	<i>ADAMTS16</i>	2.02E-08	1.18E-07	-1.52
ENSG00000126010	<i>GRPR</i>	2.09E-08	1.21E-07	-2.01
ENSG00000169126	<i>ARMC4</i>	2.31E-08	1.31E-07	-1.62
ENSG00000255026	<i>AC136475.3</i>	2.43E-08	1.36E-07	-1.55
ENSG00000167654	<i>ATCAY</i>	2.45E-08	1.36E-07	-1.89
ENSG00000067840	<i>PDZD4</i>	2.62E-08	1.44E-07	-1.72
ENSG00000274993	<i>AC254629.1</i>	2.62E-08	1.44E-07	-1.50
ENSG00000178773	<i>CPNE7</i>	2.97E-08	1.59E-07	-1.66
ENSG00000155980	<i>KIF5A</i>	2.98E-08	1.59E-07	-1.63
ENSG00000256288	<i>AC022075.3</i>	3.01E-08	1.61E-07	-1.55
ENSG00000104967	<i>NOVA2</i>	3.05E-08	1.62E-07	-1.93
ENSG00000131094	<i>CIQL1</i>	3.11E-08	1.64E-07	-1.55
ENSG00000204791	<i>SMPD5</i>	3.16E-08	1.67E-07	-1.63
ENSG00000027869	<i>SH2D2A</i>	3.34E-08	1.73E-07	-1.54

ENSG00000128274	<i>A4GALT</i>	3.43E-08	1.77E-07	-1.59
ENSG00000166448	<i>TMEM130</i>	3.44E-08	1.77E-07	-1.62
ENSG00000050767	<i>COL23A1</i>	3.59E-08	1.83E-07	-1.56
ENSG00000204264	<i>PSMB8</i>	3.63E-08	1.84E-07	-1.65
ENSG00000140675	<i>SLC5A2</i>	3.67E-08	1.85E-07	-1.54
ENSG00000162344	<i>FGF19</i>	3.81E-08	1.91E-07	-1.88
ENSG00000104888	<i>SLC17A7</i>	3.88E-08	1.93E-07	-1.73
ENSG00000168490	<i>PHYHIP</i>	4.14E-08	2.03E-07	-1.58
ENSG00000154065	<i>ANKRD29</i>	4.27E-08	2.08E-07	-1.65
ENSG00000198844	<i>ARHGEF15</i>	4.32E-08	2.09E-07	-1.53
ENSG00000072041	<i>SLC6A15</i>	4.61E-08	2.21E-07	-1.59
ENSG00000180739	<i>SIPR5</i>	4.71E-08	2.25E-07	-1.57
ENSG00000176387	<i>HSD11B2</i>	4.76E-08	2.27E-07	-1.70
ENSG00000238178	<i>AC078993.1</i>	4.80E-08	2.28E-07	-1.89
ENSG00000163958	<i>ZDHHC19</i>	4.82E-08	2.28E-07	-1.54
ENSG00000183166	<i>CALN1</i>	5.30E-08	2.45E-07	-1.68
ENSG00000277531	<i>PNMA8C</i>	5.72E-08	2.60E-07	-1.54
ENSG00000243709	<i>LEFTY1</i>	5.94E-08	2.68E-07	-2.23
ENSG00000070019	<i>GUCY2C</i>	6.85E-08	2.98E-07	-1.54
ENSG00000166816	<i>LDHD</i>	7.56E-08	3.20E-07	-1.78
ENSG00000143847	<i>PPFIA4</i>	7.74E-08	3.26E-07	-1.54
ENSG00000127241	<i>MASP1</i>	7.77E-08	3.27E-07	-1.53
ENSG00000179292	<i>TMEM151A</i>	8.37E-08	3.47E-07	-1.57
ENSG00000121871	<i>SLITRK3</i>	8.57E-08	3.54E-07	-1.90
ENSG00000110076	<i>NRXN2</i>	8.68E-08	3.57E-07	-1.59
ENSG00000162039	<i>MEIOB</i>	8.79E-08	3.60E-07	-1.76
ENSG00000101282	<i>RSPO4</i>	9.43E-08	3.81E-07	-1.53
ENSG00000236154	<i>AL450311.2</i>	9.47E-08	3.81E-07	-1.67
ENSG00000174004	<i>NRROS</i>	9.50E-08	3.82E-07	-1.56
ENSG00000204352	<i>C9orf129</i>	9.81E-08	3.91E-07	-1.83
ENSG00000109255	<i>NMU</i>	1.01E-07	3.98E-07	-1.78
ENSG00000198483	<i>ANKRD35</i>	1.08E-07	4.21E-07	-1.56
ENSG00000170925	<i>TEX13B</i>	1.14E-07	4.39E-07	-1.77
ENSG00000253230	<i>LINC00599</i>	1.14E-07	4.39E-07	-1.78
ENSG00000136449	<i>MYCBPAP</i>	1.19E-07	4.55E-07	-1.51
ENSG00000156574	<i>NODAL</i>	1.19E-07	4.58E-07	-1.95
ENSG00000147596	<i>PRDM14</i>	1.28E-07	4.82E-07	-1.93
ENSG00000078053	<i>AMPH</i>	1.30E-07	4.87E-07	-1.52
ENSG00000224729	<i>PCOLCE-ASI</i>	1.33E-07	4.96E-07	-1.56
ENSG00000141837	<i>CACNA1A</i>	1.44E-07	5.27E-07	-1.61
ENSG00000120949	<i>TNFRSF8</i>	1.48E-07	5.40E-07	-1.91
ENSG00000101194	<i>SLC17A9</i>	1.55E-07	5.62E-07	-1.74
ENSG00000178947	<i>SMIM10L2A</i>	1.59E-07	5.73E-07	-1.63
ENSG00000185668	<i>POU3F1</i>	1.62E-07	5.81E-07	-1.56
ENSG00000184408	<i>KCND2</i>	1.63E-07	5.86E-07	-1.59
ENSG00000248131	<i>LINC01194</i>	1.69E-07	6.01E-07	-2.06
ENSG00000164949	<i>GEM</i>	1.74E-07	6.16E-07	-1.53
ENSG00000176697	<i>BDNF</i>	1.96E-07	6.76E-07	-1.55
ENSG00000078295	<i>ADCY2</i>	2.06E-07	7.01E-07	-1.57
ENSG00000140835	<i>CHST4</i>	2.06E-07	7.01E-07	-1.52
ENSG00000124092	<i>CTCFL</i>	2.07E-07	7.02E-07	-1.68
ENSG00000260802	<i>SERTM2</i>	2.10E-07	7.11E-07	-1.57

ENSG00000144229	<i>THSD7B</i>	2.11E-07	7.13E-07	-1.55
ENSG00000134516	<i>DOCK2</i>	2.19E-07	7.30E-07	-1.62
ENSG00000154080	<i>CHST9</i>	2.25E-07	7.43E-07	-1.62
ENSG00000169856	<i>ONECUT1</i>	2.29E-07	7.56E-07	-1.52
ENSG00000163286	<i>ALPPL2</i>	2.37E-07	7.75E-07	-1.54
ENSG00000070886	<i>EPHA8</i>	2.46E-07	7.98E-07	-1.54
ENSG00000074370	<i>ATP2A3</i>	2.47E-07	7.99E-07	-1.65
ENSG00000128052	<i>KDR</i>	2.80E-07	8.84E-07	-1.58
ENSG00000185737	<i>NRG3</i>	2.90E-07	9.07E-07	-1.52
ENSG00000164344	<i>KLKB1</i>	2.94E-07	9.15E-07	-1.71
ENSG00000168421	<i>RHOH</i>	3.00E-07	9.30E-07	-1.83
ENSG00000204121	<i>ECEL1P1</i>	3.11E-07	9.56E-07	-1.68
ENSG00000175229	<i>GAL3ST3</i>	3.22E-07	9.82E-07	-1.56
ENSG00000157368	<i>IL34</i>	3.30E-07	1.00E-06	-1.65
ENSG00000237087	<i>AC068134.2</i>	3.39E-07	1.02E-06	-1.66
ENSG00000100341	<i>PNPLA5</i>	3.46E-07	1.04E-06	-1.60
ENSG00000155897	<i>ADCY8</i>	3.46E-07	1.04E-06	-1.81
ENSG00000136014	<i>USP44</i>	3.48E-07	1.05E-06	-1.58
ENSG00000184344	<i>GDF3</i>	3.51E-07	1.05E-06	-2.07
ENSG00000143494	<i>VASH2</i>	3.73E-07	1.10E-06	-1.51
ENSG00000150510	<i>FAM124A</i>	3.88E-07	1.14E-06	-1.59
ENSG00000117013	<i>KCNQ4</i>	3.89E-07	1.14E-06	-1.52
ENSG00000243004	<i>AC005062.1</i>	3.99E-07	1.16E-06	-1.58
ENSG00000164746	<i>C7orf57</i>	4.09E-07	1.18E-06	-1.52
ENSG00000165731	<i>RET</i>	4.11E-07	1.19E-06	-1.63
ENSG00000055118	<i>KCNH2</i>	4.22E-07	1.21E-06	-1.54
ENSG00000177238	<i>TRIM72</i>	4.24E-07	1.21E-06	-1.70
ENSG00000130303	<i>BST2</i>	4.35E-07	1.24E-06	-1.69
ENSG00000101445	<i>PPP1R16B</i>	4.44E-07	1.26E-06	-1.52
ENSG00000179761	<i>PIPOX</i>	4.50E-07	1.27E-06	-1.66
ENSG00000069482	<i>GAL</i>	4.58E-07	1.29E-06	-1.86
ENSG00000080573	<i>COL5A3</i>	4.68E-07	1.32E-06	-1.72
ENSG00000146215	<i>CRIP3</i>	5.12E-07	1.41E-06	-1.55
ENSG00000159674	<i>SPON2</i>	5.18E-07	1.42E-06	-1.56
ENSG00000100167	<i>SEPT3</i>	5.19E-07	1.42E-06	-1.54
ENSG00000196189	<i>SEMA4A</i>	5.30E-07	1.45E-06	-1.67
ENSG00000137571	<i>SLCO5A1</i>	5.40E-07	1.47E-06	-1.73
ENSG00000156475	<i>PPP2R2B</i>	5.57E-07	1.50E-06	-1.51
ENSG00000151952	<i>TMEM132D</i>	5.88E-07	1.57E-06	-1.55
ENSG00000157782	<i>CABP1</i>	6.11E-07	1.62E-06	-1.56
ENSG00000090339	<i>ICAM1</i>	7.14E-07	1.85E-06	-1.66
ENSG00000257474	<i>AC027288.1</i>	8.57E-07	2.13E-06	-1.70
ENSG00000170703	<i>TTL6</i>	8.77E-07	2.17E-06	-1.59
ENSG00000104327	<i>CALB1</i>	9.73E-07	2.36E-06	-1.75
ENSG00000129244	<i>ATP1B2</i>	1.04E-06	2.48E-06	-1.70
ENSG00000160973	<i>FOXH1</i>	1.14E-06	2.67E-06	-1.58
ENSG00000131969	<i>ABHD12B</i>	1.19E-06	2.76E-06	-1.70
ENSG00000151224	<i>MAT1A</i>	1.22E-06	2.82E-06	-1.74
ENSG00000101180	<i>HRH3</i>	1.28E-06	2.92E-06	-1.60
ENSG00000204936	<i>CD177</i>	1.41E-06	3.16E-06	-1.52
ENSG00000074527	<i>NTN4</i>	1.48E-06	3.30E-06	-1.52
ENSG00000261115	<i>TMEM178B</i>	1.49E-06	3.31E-06	-1.52

ENSG00000107831	<i>FGF8</i>	1.59E-06	3.50E-06	-1.74
ENSG00000113763	<i>UNC5A</i>	1.60E-06	3.51E-06	-1.68
ENSG00000015413	<i>DPEP1</i>	1.69E-06	3.68E-06	-1.59
ENSG00000254277	<i>AC009446.1</i>	2.03E-06	4.24E-06	-1.63
ENSG00000196361	<i>ELAVL3</i>	2.07E-06	4.32E-06	-1.65
ENSG00000171794	<i>UTF1</i>	2.14E-06	4.43E-06	-1.93
ENSG00000173175	<i>ADCY5</i>	2.21E-06	4.56E-06	-1.51
ENSG00000225783	<i>MIAT</i>	2.27E-06	4.64E-06	-1.73
ENSG00000172731	<i>LRRC20</i>	2.30E-06	4.71E-06	-1.51
ENSG00000254934	<i>LINC00678</i>	2.36E-06	4.82E-06	-2.09
ENSG00000265992	<i>ESRG</i>	2.49E-06	5.03E-06	-1.66
ENSG00000232301	<i>LNCPRESS1</i>	2.57E-06	5.15E-06	-1.72
ENSG00000117643	<i>MANIC1</i>	2.60E-06	5.20E-06	-1.53
ENSG00000187608	<i>ISG15</i>	2.73E-06	5.42E-06	-1.54
ENSG00000234965	<i>SHISA8</i>	2.81E-06	5.56E-06	-1.51
ENSG00000196092	<i>PAX5</i>	3.08E-06	5.99E-06	-1.72
ENSG00000198963	<i>RORB</i>	3.13E-06	6.05E-06	-1.72
ENSG00000185885	<i>IFITM1</i>	3.48E-06	6.61E-06	-1.57
ENSG00000226792	<i>C13orf42</i>	3.54E-06	6.73E-06	-1.71
ENSG00000121207	<i>LRAT</i>	3.85E-06	7.21E-06	-1.82
ENSG00000230798	<i>FOXD3-AS1</i>	3.92E-06	7.32E-06	-1.82
ENSG00000105605	<i>CACNG7</i>	3.99E-06	7.41E-06	-1.56
ENSG00000196159	<i>FAT4</i>	4.22E-06	7.75E-06	-1.57
ENSG00000187569	<i>DPPA3</i>	4.35E-06	7.96E-06	-1.57
ENSG00000173227	<i>SYT12</i>	4.40E-06	8.04E-06	-1.53
ENSG00000151789	<i>ZNF385D</i>	4.43E-06	8.07E-06	-1.53
ENSG00000253507	<i>AC104257.1</i>	4.78E-06	8.60E-06	-2.04
ENSG00000244342	<i>LINC00698</i>	4.85E-06	8.72E-06	-1.60
ENSG00000177108	<i>ZDHHC22</i>	5.16E-06	9.18E-06	-1.56
ENSG00000134917	<i>ADAMTS8</i>	5.32E-06	9.39E-06	-1.57
ENSG00000178233	<i>TMEM151B</i>	5.38E-06	9.48E-06	-1.58
ENSG00000151650	<i>VENTX</i>	5.52E-06	9.67E-06	-1.69
ENSG00000133454	<i>MYO18B</i>	6.17E-06	1.06E-05	-1.51
ENSG00000165140	<i>FBP1</i>	6.45E-06	1.10E-05	-1.65
ENSG00000187140	<i>FOXD3</i>	6.73E-06	1.14E-05	-1.86
ENSG00000119138	<i>KLF9</i>	7.13E-06	1.20E-05	-1.62
ENSG00000182050	<i>MGAT4C</i>	7.68E-06	1.27E-05	-1.85
ENSG00000173673	<i>HES3</i>	7.97E-06	1.31E-05	-1.86
ENSG00000188816	<i>HMX2</i>	9.23E-06	1.48E-05	-1.65
ENSG00000255794	<i>RMST</i>	9.42E-06	1.50E-05	-1.73
ENSG00000116833	<i>NR5A2</i>	1.01E-05	1.59E-05	-1.57
ENSG00000122859	<i>NEUROG3</i>	1.10E-05	1.71E-05	-1.66
ENSG00000139209	<i>SLC38A4</i>	1.12E-05	1.73E-05	-1.53
ENSG00000043355	<i>ZIC2</i>	1.30E-05	1.96E-05	-1.56
ENSG00000224557	<i>HLA-DPB2</i>	1.32E-05	1.99E-05	-1.64
ENSG00000048540	<i>LMO3</i>	1.43E-05	2.12E-05	-1.79
ENSG00000166473	<i>PKD1L2</i>	1.44E-05	2.14E-05	-1.80
ENSG00000124493	<i>GRM4</i>	1.47E-05	2.17E-05	-1.56
ENSG00000140853	<i>NLRC5</i>	1.74E-05	2.50E-05	-1.53
ENSG00000165810	<i>BTNL9</i>	2.12E-05	2.97E-05	-1.55
ENSG00000095370	<i>SH2D3C</i>	2.55E-05	3.47E-05	-1.59
ENSG00000171388	<i>APLN</i>	2.61E-05	3.54E-05	-1.65

ENSG00000166105	<i>GLB1L3</i>	2.65E-05	3.59E-05	-1.73
ENSG00000130477	<i>UNC13A</i>	3.15E-05	4.15E-05	-1.55
ENSG00000183049	<i>CAMK1D</i>	3.23E-05	4.25E-05	-1.50
ENSG00000163735	<i>CXCL5</i>	3.48E-05	4.51E-05	-1.51
ENSG00000260834	<i>AC009055.2</i>	3.57E-05	4.61E-05	-1.66
ENSG00000164128	<i>NPY1R</i>	3.59E-05	4.63E-05	-1.56
ENSG00000095587	<i>TLL2</i>	4.04E-05	5.14E-05	-1.56
ENSG00000248215	<i>LINC02505</i>	4.87E-05	6.01E-05	-1.54
ENSG00000164076	<i>CAMKV</i>	4.93E-05	6.07E-05	-1.64
ENSG00000131771	<i>PPP1R1B</i>	6.48E-05	7.67E-05	-1.52
ENSG00000177468	<i>OLIG3</i>	6.58E-05	7.77E-05	-1.68
ENSG00000169896	<i>ITGAM</i>	6.74E-05	7.92E-05	-1.50
ENSG00000261780	<i>LINC02582</i>	6.77E-05	7.94E-05	-1.68
ENSG00000168447	<i>SCNN1B</i>	8.34E-05	9.52E-05	-1.59
ENSG00000125730	<i>C3</i>	8.59E-05	9.76E-05	-1.53
ENSG00000234787	<i>LINC00458</i>	8.80E-05	9.97E-05	-1.60
ENSG00000167178	<i>ISLR2</i>	9.64E-05	1.08E-04	-1.70
ENSG00000215866	<i>LINC01356</i>	1.04E-04	1.15E-04	-1.50
ENSG00000271601	<i>LIX1L</i>	1.33E-04	1.43E-04	-1.55
ENSG00000197587	<i>DMBX1</i>	1.41E-04	1.51E-04	-1.54
ENSG00000158473	<i>CD1D</i>	2.58E-04	2.53E-04	-1.51
ENSG00000184515	<i>BEX5</i>	3.30E-04	3.12E-04	-1.54
ENSG00000255666	<i>AP000943.2</i>	4.76E-04	4.29E-04	-1.63
ENSG00000214575	<i>CPEB1</i>	9.39E-04	7.75E-04	-1.51
ENSG00000166869	<i>CHP2</i>	1.09E-03	8.85E-04	-1.51
ENSG00000130513	<i>GDF15</i>	2.98E-03	2.14E-03	-1.57

Supplemental Table S3. Gene ontology (GO) categories identified as associated (p-value<0.01) with genes expressed at significantly higher expression levels in differentiated vs. undifferentiated hESCs. Gene ontology categories are listed along with their respective p-values of enrichment, false discovery rate (FDR)-adjusted p-values of enrichment, and specific genes relevant to each gene ontology category.

Gene Ontology Category	p-value	FDR-adjusted p-value	Number of Genes with Significantly Higher Expression in Differentiated vs. Undifferentiated hESCs within GO Category	Genes with Significantly Higher Expression in Differentiated vs. Undifferentiated hESCs within GO Category
GO_ANIMAL_ORGAN_MORPHOGENESIS	1.43E-21	1.43E-17	63	ACTC1, ALDH1A2, ANKRD1, BARX2, CDX2, COL11A1, COL3A1, CSF1R, CSGALNACT1, DIO3, DLX1, DLX2, DLX3, DLX5, DLX6, EFNA1, FOLR1, GATA2, GATA3, GREB1L, GRHL3, HAND1, HEY1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, HOXC13, ID4, INHBA, ISL1, LEF1, LRP2, MEIS1, MSX1, MSX2, NOG, OSR1, PDX1, SLC40A1, SLC6A4, SNAI2, SOX9, SP5, SP6, TACSTD2, TBX3, TCF21, TFAP2A, TFAP2B, TGM2, TNC, TP63, TWIST1, VIT, WNT3A, WNT4, WNT6, WNT9B
GO_EMBRYONIC_MORPHOGENESIS	2.60E-20	1.30E-16	46	ALDH1A2, AMOT, COL11A1, DLX1, DLX2, DLX3, DLX6, EFNA1, EYA2, FLRT3, FOLR1, GATA2, GATA3, GREM2, GRHL3, HAND1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, INHBA, LAMB3, LEF1, LRP2, MSX1, MSX2, NOG, OSR1, PDX1, PITX1, SOX7, SOX9, TBX3, TCF21, TFAP2A, TP63, TWIST1, WLS, WNT3A, WNT4, WNT6, WNT9B, ZEB2
GO_ANATOMICAL_STRUCTURE_FORMATION_INVOLVED_IN_MORPHOGENESIS	4.17E-20	1.39E-16	65	ACKR3, ACTC1, ADGRG1, ALDH1A2, AMOT, ANKRD1, ANXA1, BMPER, CASQ2, CDX2, COL11A1, CYP1B1, DLX1, DLX3, DLX6, EFNA1, ENPEP, EPAS1, EYA2, FGFBP1, FOLR1, GATA2, GATA3, GRHL3, HAND1, HEY1, HOXB3, IL18, INHBA, ISL1, LAMB3, LEF1, LMOD2, LRP2, MEIS1, MSX1, MSX2, MYLK3, MYOF, NOG, NPPB, OSR1, PLXNA2, PPARG, PRKD1, RUNX1, SLC40A1, SNAI2, SOX7, SOX9, SPHK1, TBX3, TCF21, TFAP2A, TFAP2B, TGM2, THSD7A, TP63, TWIST1, WLS, WNT3A, WNT4, WNT6, WNT9B, ZEB2
GO_TISSUE_MORPHOGENESIS	9.39E-19	2.35E-15	47	ACTC1, ALDH1A2, ANKRD1, COL11A1, COL3A1, CSF1R, DLX1, EYA2, FLRT3, FOLR1, GATA3, GREB1L, GRHL3, HAND1, HEY1, HOXB2, HOXB4, HOXB7, ID4, INHBA, ISL1, KRT16, KRT17, LEF1, LRP2, MSX1, MSX2, NOG, OSR1, PDX1, SNAI2, SOX9, TACSTD2, TBX3, TCF21, TFAP2A, TGM2, TNC, TP63, TWIST1, VIT, WLS, WNT3A, WNT4, WNT6, WNT9B, ZEB2
GO_EMBRYO_DEVELOPMENT	2.26E-18	4.52E-15	57	ALDH1A2, AMOT, CDX2, COL11A1, DLX1, DLX2, DLX3, DLX6, EFNA1, EN2, EPAS1, EVX1, EYA2, FLRT3, FOLR1, GATA2, GATA3, GREM2, GRHL3, HAND1, HEY1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, HOXB9, INHBA, ISL1, LAMB3, LEF1, LRP2, MSX1, MSX2, NOG, NR2F2, OSR1, PDX1, PITX1, PLPP4, PLXNA2, SOX7, SOX9, TBX3, TCF21, TFAP2A, TP63, TWIST1, WLS, WNT3A, WNT4, WNT6, WNT9B, ZEB2
GO_TUBE_MORPHOGENESIS	1.68E-16	2.80E-13	52	ACKR3, ADGRG1, AMOT, ANXA1, BMPER, COL3A1, CSF1R, CYP1B1, DLX1, EFNA1, ENPEP, EPAS1, FGFBP1, FOLR1, GATA2, GATA3, GREB1L, GRHL3, HAND1, HEY1, HOXB3, HOXB7, IL18, ISL1, LEF1, LRP2, MEIS1, MSX2, MYOCD, NOG, NPPB, NR2F2, OSR1, PPARG, PRKD1, RUNX1, SOX9, SPHK1, TACSTD2, TBX3, TCF21, TFAP2B, TGM2, THSD7A, TNC, TP63, TWIST1, WNT3A, WNT4, WNT6, WNT9B, ZEB2
GO_PATTERN_SPECIFICATION_PROCESS	9.75E-16	1.39E-12	35	ADGRG1, ALDH1A2, CDX2, DLX1, DLX2, DMRTA2, EVX1, FOLR1, GREM2, GRHL3, HAND1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, HOXB9, HOXC13, ISL1, LEF1, LRP2, MSX1, MSX2, NOG, NR2F2, OSR1, PLXNA2, TBX3, TP63, WLS, WNT3A, WNT6, ZEB2
GO_TUBE_DEVELOPMENT	1.40E-15	1.75E-12	56	ACKR3, ADGRG1, ALDH1A2, AMOT, ANXA1, BMPER, CDX2, COL3A1, CSF1R, CYP1B1, DLX1, EFNA1, ENPEP, EPAS1, FGFBP1, FOLR1, GATA2, GATA3, GREB1L, GRHL3, HAND1, HEY1, HOXB3, HOXB7, IL18, ISL1, LEF1, LRP2, MEIS1, MSX2, MYOCD, NOG, NPPB, NR2F2, OSR1, PDX1, PLXNA2, PPARG, PRKD1, RUNX1, SOX9, SPHK1, TACSTD2, TBX3, TCF21, TFAP2B, TGM2, THSD7A, TNC, TP63, TWIST1, WNT3A, WNT4, WNT6, WNT9B, ZEB2
GO_REGIONALIZATION	1.69E-15	1.88E-12	31	ADGRG1, ALDH1A2, CDX2, DLX1, DLX2, DMRTA2, EVX1, GREM2, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, HOXB9, HOXC13, ISL1, LEF1, LRP2, MSX1, MSX2, NOG, NR2F2, OSR1, PLXNA2, TBX3, TP63, WLS, WNT3A, ZEB2
GO_EMBRYONIC_ORGAN_DEVELOPMENT	2.49E-15	2.49E-12	34	ALDH1A2, CDX2, COL11A1, DLX2, DLX3, DLX6, EFNA1, EN2, EPAS1, FOLR1, GATA2, GATA3, GRHL3, HAND1, HEY1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, LEF1, MSX1, NOG, NR2F2, OSR1, SOX9, TBX3, TCF21, TFAP2A, TWIST1, WNT3A, WNT9B
GO_CIRCULATORY_SYSTEM_DEVELOPMENT	2.98E-15	2.71E-12	57	ACKR3, ACTC1, ADGRG1, ALDH1A2, AMOT, ANKRD1, ANXA1, BMPER, CDX2, COL11A1, COL3A1, CYP1B1, DLX1, DLX3, EFNA1, ENPEP, EPAS1, FGFBP1, FLRT3, FOLR1, GATA2, GATA3, GPER1, GREB1L, HAND1, HEY1, HOXB3, IL18, ISL1, JPH2, LEF1, LRP2, MEIS1, MSX1, MSX2, MYLK3, MYOCD, NOG, NPPB, NR2F2, OSR1, POPDC2, PPARG, PRKD1, RUNX1, SGC6, SLC8A1, SNAI2, SOX9, SPHK1, TBX3, TCF21, TFAP2B, THSD7A, TWIST1, WNT3A, WNT4
GO_EPITHELIUM_DEVELOPMENT	3.63E-15	3.02E-12	60	ALDH1A2, ANXA1, BMPER, CDX2, CSF1R, DLX1, DLX3, DLX5, DLX6, FLRT3, FOLR1, GATA3, GREB1L, GRHL3, HAND1, HEY1, HOXB2, HOXB4, HOXB5, HOXB7, HOXC13, ID4, INHBA, KRT16, KRT17, KRT23, KRT80, LEF1, LRP2, MSX1, MSX2, NOG, NR2F2, OSR1, PDX1, PLXNA2, PPARG, RUNX1, SLC40A1, SNAI2, SOX9, TACSTD2, TBX3, TCF21, TFAP2A, TFAP2B, TGM1, TGM2, TNC, TNFRSF19, TP63, TWIST1, UPK2, WNT3A, WNT4, WNT5B, WNT6, WNT9B, ZEB2, ZNF703
GO_SKELETAL_SYSTEM_DEVELOPMENT	5.38E-15	4.14E-12	37	BARX2, COL11A1, COL19A1, COL3A1, CSGALNACT1, DLX1, DLX2, DLX3, DLX6, GDF6, HAND1, HAPLN1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, HOXB9, LUM, MEIS1, MSX1, MSX2, NOG, OSR1, PITX1, SNAI2, SOX9, SP5, TBX3, TFAP2A, TP63, TWIST1, VIT, WNT5B, WNT9B
GO_EMBRYONIC_ORGAN_MORPHOGENESIS	3.85E-14	2.75E-11	27	COL11A1, DLX2, DLX3, DLX6, EFNA1, FOLR1, GATA2, GATA3, GRHL3, HAND1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, MSX1, NOG, OSR1, SOX9, TBX3, TCF21, TFAP2A, TWIST1, WNT3A, WNT9B
GO_MORPHOGENESIS_OF_AN_EPITHELIUM	5.03E-14	3.35E-11	36	ALDH1A2, CSF1R, DLX1, FLRT3, FOLR1, GATA3, GREB1L, GRHL3, HAND1, HOXB2, HOXB4, HOXB7, ID4, KRT16, KRT17, LEF1, LRP2, MSX2, NOG, OSR1, PDX1, SNAI2, SOX9, TACSTD2, TBX3, TCF21, TFAP2A, TGM2, TNC, TP63, TWIST1, WNT3A, WNT4, WNT6, WNT9B, ZEB2
GO_EMBRYO_DEVELOPMENT_ENDING_IN_BIRTH_OR_EGG_HATCHING	7.21E-14	4.50E-11	39	ALDH1A2, AMOT, CDX2, COL11A1, DLX1, DLX2, EPAS1, EVX1, FOLR1, GATA2, GATA3, GRHL3, HAND1, HEY1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, HOXB9, ISL1, LEF1, LRP2, MSX1, NOG, NR2F2, OSR1, PLPP4, PLXNA2, SOX9, TBX3, TFAP2A, TWIST1, WNT3A, WNT9B, ZEB2
GO_SEQUENCE_SPECIFIC_DNA_BINDING	5.40E-13	3.18E-10	52	BARX2, CDX2, DLX1, DLX2, DLX3, DLX5, DLX6, DMRTA2, EN2, EPAS1, EVX1, GATA2, GATA3, GRHL3, HAND1, HEY1, HMX1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, HOXB9, HOXC13, HR, ISL1, LEF1, MEIS2, MSX1, MSX2, MYOCD, NR2F2, OSR1, PDX1, PITX1, PPARG, PRDM6, RUNX1, SNAI2, SOX9, SP5, TBX3, TCF21, TFAP2A, TFAP2B, TP63, TWIST1, ZEB2, ZNF750

GO_ANTERIOR_POSTERIOR_PATTERN_SPECIFICATION	1.52E-12	8.41E-10	22	ALDH1A2, CDX2, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, HOXB9, HOXC13, LEF1, MSX1, MSX2, NOG, NR2F2, OSR1, PLXNA2, TBX3, WLS, WNT3A, ZEB2
GO_MESENCHYME_MORPHOGENESIS	7.27E-12	3.83E-09	12	ACTC1, HEY1, ISL1, LEF1, MSX1, MSX2, NOG, OSR1, SNAI2, SOX9, TWIST1, WNT3A
GO_MUSCLE_STRUCTURE_DEVELOPMENT	8.51E-12	4.25E-09	37	ACTC1, ANKRD1, BARX2, CASQ2, COL11A1, COL19A1, COL3A1, DMRTA2, EPAS1, GPER1, HAND1, HEY1, IGFBP3, IL18, ISL1, JPH2, LEF1, LMOD2, LRP2, MEIS1, MSX1, MYLK3, MYOCD, MYOF, NOG, NR2F2, PITX1, POPDC2, PRDM6, SGC6, SLC8A1, SOX9, TBX3, TCF21, TWIST1, WNT3A, WNT4
GO_DNA_BINDING_TRANSCRIPTION_ACTIVATOR_ACTIVITY	9.66E-12	4.60E-09	29	BARX2, DLX2, DLX3, DLX5, EPAS1, GATA2, GATA3, GRHL3, HOXB2, HOXB3, HOXB4, HOXB5, HOXB7, HOXC13, ISL1, LEF1, MEIS1, MEIS2, MSX1, MYOCD, PITX1, RUNX1, SOX9, TCF21, TFAP2A, TFAP2B, TP63, ZEB2, ZNF750
GO_MORPHOGENESIS_OF_EMBRYONIC_EPITHELIUM	1.44E-11	6.54E-09	18	ALDH1A2, DLX1, FOLR1, GATA3, GRHL3, HAND1, LRP2, NOG, OSR1, PDX1, SOX9, TFAP2A, TP63, TWIST1, WNT4, WNT6, WNT9B, ZEB2
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_II	1.57E-11	6.84E-09	51	BARX2, CDKN2B, DLX1, DLX2, DLX3, DLX5, DLX6, EN2, EPAS1, EVX1, GATA2, GATA3, GPER1, GRHL3, HAND1, HEY1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB7, HOXB8, HOXC13, ID4, IL18, INHBA, ISL1, LEF1, LUM, MEIS1, MEIS2, MSX1, MYOCD, NOG, OSR1, PDX1, PITX1, PPARG, PRKD1, RUNX1, SLC40A1, SMAD9, SOX9, TCF21, TFAP2A, TFAP2B, TP63, TWIST1, WNT3A, ZEB2, ZNF750
GO_SKELETAL_SYSTEM_MORPHOGENESIS	1.69E-11	7.04E-09	22	BARX2, COL11A1, CSGALNACT1, DLX2, DLX5, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, MSX1, MSX2, NOG, OSR1, SOX9, SP5, TFAP2A, TWIST1, VIT, WNT9B
GO_SEQUENCE_SPECIFIC_DOUBLE_STRANDED_DNA_BINDING	3.12E-11	1.25E-08	42	BARX2, CDX2, DLX1, DLX2, DLX3, DLX5, DLX6, GATA2, GATA3, HAND1, HEY1, HMV1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, HR, ISL1, LEF1, MEIS1, MEIS2, MSX1, MSX2, MYOCD, OSR1, PDX1, PITX1, PPARG, PRDM6, RUNX1, SNAI2, SOX9, SP5, TBX3, TCF21, TFAP2A, TFAP2B, TWIST1, ZNF750
GO_REGULATORY_REGION_NUCLEIC_ACID_BINDING	3.30E-11	1.27E-08	44	BARX2, CDX2, DLX1, DLX2, DLX3, DLX5, DLX6, GATA2, GATA3, HAND1, HEY1, HMV1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, HR, ISL1, LEF1, MEIS1, MEIS2, MSX1, MSX2, MYOCD, OSR1, PDX1, PITX1, PPARG, PRDM6, RUNX1, SNAI2, SOX7, SOX9, SP5, TBX3, TCF21, TFAP2A, TFAP2B, TP63, TWIST1, ZNF750
GO_CENTRAL_NERVOUS_SYSTEM_DEVELOPMENT	3.61E-11	1.30E-08	45	ADGRG1, ALDH1A2, CNTN4, COL3A1, CSF1R, DLX1, DLX2, DLX5, DMRTA2, EN2, EVX1, GATA2, GRHL3, HAPLN1, HOXB2, HOXB3, HOXB8, ID4, INHBA, ISL1, LEF1, LRP2, MAL, MSX1, NOG, NR2F2, PDX1, PITX1, PLXNA2, PPARG, SEMA6D, SLC6A4, SLC8A1, SOX9, SPHK1, TBX3, TFAP2A, UNC5C, VIT, WLS, WNT3A, WNT4, WNT9B, ZEB2
GO_MUSCLE_TISSUE_DEVELOPMENT	3.63E-11	1.30E-08	28	ACTC1, ALDH1A2, ANKRD1, COL11A1, COL19A1, COL3A1, DMRTA2, EYA2, HAND1, ISL1, JPH2, LEF1, LRP2, MEIS1, MYLK3, MYOCD, NOG, NR2F2, OSR1, PITX1, POPDC2, SGC6, SLC8A1, SOX9, TBX3, TCF21, TWIST1, WNT3A
GO_CARDIOVASCULAR_SYSTEM_DEVELOPMENT	5.04E-11	1.74E-08	40	ACKR3, ADGRG1, ALDH1A2, AMOT, ANXA1, BMPER, CDX2, COL3A1, CYP1B1, DLX3, EFNA1, ENPEP, EPAS1, FGFBP1, FOLR1, GATA2, GPER1, HAND1, HEY1, HOXB3, IL18, ISL1, LEF1, LRP2, MEIS1, MYOCD, NOG, NPPB, NR2F2, OSR1, PPARG, PRKD1, RUNX1, SPHK1, TBX3, TCF21, TFAP2B, THSD7A, TWIST1, WNT4
GO_POSITIVE_REGULATION_OF_RNA_BIOSYNTHETIC_PROCESSES	5.46E-11	1.82E-08	60	AFAP1L2, ANKRD1, BARX2, CDKN2B, CDX2, DLX1, DLX2, DLX3, DLX5, DLX6, EN2, EPAS1, EVX1, GATA2, GATA3, GDF6, GPER1, GRHL3, HAND1, HEY1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB7, HOXB8, HOXC13, ID4, IL18, INHBA, ISL1, LEF1, LUM, MEIS1, MEIS2, MSX1, MYOCD, NOG, NR2F2, OSR1, PDX1, PITX1, PPARG, PRKD1, RUNX1, SLC40A1, SMAD9, SOX9, TBX3, TCF21, TFAP2A, TFAP2B, TP63, TWIST1, VGLL1, WNT3A, WNT4, WNT6, ZEB2, ZNF750
GO_NEGATIVE_REGULATION_OF_CELL_DIFFERENTIATION	6.27E-11	2.01E-08	38	ADGRG1, ANXA1, CNTN4, COL3A1, DIO3, DLX1, DLX2, EFNA1, GATA2, GATA3, GPER1, HOXB8, ID4, IL18, INHBA, ISL1, MEIS1, MEIS2, MSX1, MSX2, MYOCD, NOG, OSR1, POSTN, PPARG, PRDM6, PRTG, RUNX1, SEMA6D, SLC6A4, SNAI2, SOX9, TACSTD2, TBX3, TP63, TWIST1, WNT3A, WNT4
GO_HEART_DEVELOPMENT	6.45E-11	2.01E-08	33	ACTC1, ALDH1A2, ANKRD1, COL11A1, COL3A1, DLX1, EFNA1, FLRT3, FOLR1, GATA3, GPER1, GREB1L, HAND1, HEY1, ISL1, JPH2, LRP2, MEIS1, MSX1, MSX2, MYLK3, MYOCD, NOG, OSR1, POPDC2, PPARG, SGC6, SLC8A1, SNAI2, SOX9, TBX3, TWIST1, WNT3A
GO_EMBRYONIC_SKELETAL_SYSTEM_DEVELOPMENT	9.36E-11	2.83E-08	16	COL11A1, DLX1, DLX2, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, HOXB9, NOG, OSR1, TFAP2A, TWIST1, WNT9B
GO_EPITHELIAL_TUBE_MORPHOGENESIS	1.09E-10	3.19E-08	24	CSF1R, DLX1, FOLR1, GATA3, GREB1L, GRHL3, HAND1, HOXB7, LEF1, LRP2, MSX2, NOG, OSR1, SOX9, TACSTD2, TBX3, TCF21, TNC, TWIST1, WNT3A, WNT4, WNT6, WNT9B, ZEB2
GO_EMBRYONIC_SKELETAL_SYSTEM_MORPHOGENESIS	1.63E-10	4.66E-08	14	COL11A1, DLX2, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, NOG, OSR1, TFAP2A, TWIST1, WNT9B
GO_HEAD_DEVELOPMENT	1.97E-10	5.46E-08	38	ADGRG1, ALDH1A2, CNTN4, COL3A1, CSF1R, DLX1, DLX2, DLX5, DLX6, DMRTA2, EN2, FLRT3, GATA2, HOXB2, HOXB3, ID4, INHBA, ISL1, LEF1, LRP2, MSX1, NOG, NR2F2, PITX1, PLXNA2, SEMA6D, SLC6A4, SLC8A1, SOX9, SPHK1, TBX3, UNC5C, WLS, WNT3A, WNT4, WNT9B, ZEB2
GO_DOUBLE_STRANDED_DNA_BINDING	2.06E-10	5.57E-08	43	BARX2, CDX2, DLX1, DLX2, DLX3, DLX5, DLX6, GATA2, GATA3, HAND1, HEY1, HMV1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, HR, ISL1, LEF1, MEIS1, MEIS2, MSX1, MSX2, MYOCD, OSR1, PDX1, PITX1, PPARG, PRDM6, RUNX1, SNAI2, SOX9, SP5, TBX3, TCF21, TFAP2A, TFAP2B, TP63, TWIST1, ZNF750
GO_APPENDAGE_DEVELOPMENT	2.59E-10	6.82E-08	18	ALDH1A2, DLX5, DLX6, HOXC13, LEF1, MSX1, MSX2, NOG, NR2F2, OSR1, PITX1, PLXNA2, SOX9, TBX3, TFAP2A, TFAP2B, TP63, TWIST1
GO_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	7.06E-10	1.81E-07	44	ADGRG1, AMOT, ANXA1, ARHGDIB, CCR1, CNTN4, COL3A1, DIO3, DLX1, DLX2, EFNA1, GATA2, GATA3, GPER1, HOXB8, ID4, IL18, INHBA, ISL1, LEF1, MEIS1, MEIS2, MSX1, MSX2, MYOCD, NOG, NPPB, OSR1, POSTN, PPARG, PRDM6, PRTG, RUNX1, SEMA6D, SLC6A4, SNAI2, SOX9, TACSTD2, TBX3, TP63, TWIST1, WNT3A, WNT4, WNT9B
GO_GLAND_DEVELOPMENT	8.55E-10	2.14E-07	27	ALDH1A2, ANXA1, CSF1R, GATA2, GATA3, HOXB3, HOXB8, ID4, ISL1, LEF1, MSX1, MSX2, NOG, PDX1, PITX1, PRLR, SNAI2, SOX9, TBX3, TCF21, TGM2, TNC, TP63, WLS, WNT3A, WNT4, ZNF703
GO_SENSORY_ORGAN_DEVELOPMENT	9.52E-10	2.18E-07	30	ADAMTS18, ALDH1A2, BMPER, COL11A1, CYP1B1, DIO3, DLX1, DLX2, DLX5, DLX6, GATA2, GATA3, GRHL3, HOXC13, INHBA, LEF1, MEIS1, MEIS2, MSX1, NOG, OSR1, SOX9, TFAP2A, TFAP2B, TWIST1, WNT3A, WNT5B, WNT6, WNT9B, ZEB2
GO_ROOF_OF_MOUTH_DEVELOPMENT	9.54E-10	2.18E-07	13	DLX5, DLX6, INHBA, LEF1, MSX1, OSR1, SNAI2, TBX3, TCF21, TFAP2A, TWIST1, WNT3A, WNT9B
GO_POSITIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	9.56E-10	2.18E-07	53	AMOT, ANKRD1, ANXA1, BMPER, CCR1, CD274, CDX2, CLSTN2, CYP1B1, DIO3, DLX1, DLX2, DMRTA2, FGFBP1, FLRT3, GATA2, GATA3, GDF6, GPER1, HOXB4, HOXB7, ID4, IGFBP3, IL18, INHBA, ISL1, LEF1, LPL, LRP2, MSX2, MYLK3, MYOCD, NOG, OSR1, PLXNA2, PPARG, PRKD1, RUNX1, SLC8A1, SNAI2, SOX9, SPHK1, TACSTD2, TFAP2A, TP63, TWIST1, WNT3A, WNT4, WNT5B, WNT6, ZEB2, ZNF703, ZNF804A
GO_APPENDAGE_MORPHOGENESIS	9.58E-10	2.18E-07	16	ALDH1A2, DLX5, DLX6, LEF1, MSX1, MSX2, NOG, OSR1, PITX1, PLXNA2, SOX9, TBX3, TFAP2A, TFAP2B, TP63, TWIST1

GO_ODONTOGENESIS	1.03E-09	2.28E-07	15	DLX1, DLX2, DLX3, HAND1, INHBA, LEF1, MSX1, MSX2, OSR1, SP6, TFAP2A, TNC, TP63, TWIST1, WNT6
GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_II	1.12E-09	2.43E-07	38	ANKRD1, BARKX2, CDX2, DLX1, DLX2, EFN1, GATA2, GATA3, HAND1, HEY1, HMX1, HOXB3, HOXB4, HOXB8, ID4, ISL1, LEF1, MEIS2, MSX1, MSX2, MYOCD, NOG, NR2F2, OSR1, PDX1, PPARG, RUNX1, SNAI2, SOX7, SOX9, SP5, TBX3, TCF21, TFAP2A, TFAP2B, TP63, TWIST1, ZEB2
GO_BLOOD_VESSEL_MORPHOGENESIS	1.44E-09	3.07E-07	34	ACKR3, ADGRG1, AMOT, ANXA1, BMPER, COL3A1, CYP1B1, EFN1, ENPEP, EPAS1, FGFBP1, FOLR1, GATA2, HAND1, HEY1, HOXB3, IL18, ISL1, LEF1, LRP2, MEIS1, MYOCD, NOG, NPPB, NR2F2, PPARG, PRKD1, RUNX1, SPHK1, TCF21, TFAP2B, THSD7A, TWIST1, WNT4
GO_STEM_CELL_DIFFERENTIATION	1.62E-09	3.37E-07	20	ALDH1A2, FOLR1, GATA2, GATA3, HOXB4, ISL1, MSX1, MSX2, MYOCD, OSR1, PDX1, RUNX1, SEMA6D, SNAI2, SOX9, TACSTD2, TP63, TWIST1, WNT3A, ZEB2
GO_MESENCHYME_DEVELOPMENT	1.80E-09	3.67E-07	21	ACTC1, ALDH1A2, EFN1, FOLR1, HAND1, HEY1, ISL1, LEF1, MSX1, MSX2, NOG, OSR1, SEMA6D, SNAI2, SOX9, TCF21, TWIST1, WNT3A, WNT4, ZEB2, ZNF703
GO_HEART_MORPHOGENESIS	2.62E-09	5.25E-07	20	ACTC1, ALDH1A2, ANKRD1, COL11A1, DLC1, EFN1, FOLR1, GATA3, HAND1, HEY1, ISL1, LRP2, MSX1, MSX2, NOG, SNAI2, SOX9, TBX3, TWIST1, WNT3A
GO_REPRODUCTIVE_SYSTEM_DEVELOPMENT	2.94E-09	5.77E-07	26	ADGRG1, ANXA1, CDX2, DLX3, EPAS1, GATA2, GATA3, GREB1L, HAND1, HEY1, ID4, INHBA, LEF1, LRP2, MYOCD, NOG, NR2F2, OSR1, PPARG, SOX9, TBX3, TCF21, TNC, TP63, WNT4, WNT9B
GO_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY	4.48E-09	8.62E-07	58	BARKX2, BNC1, CDX2, DLX1, DLX2, DLX3, DLX5, DLX6, DMRTA2, EN2, EPAS1, EVX1, GATA2, GATA3, GRHL3, HAND1, HEY1, HMX1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB6, HOXB7, HOXB8, HOXB9, HOXC13, HR, ID4, ISL1, LEF1, MEIS1, MEIS2, MSX1, MSX2, MYOCD, NR2F2, OSR1, PDX1, PITX1, PPARG, PRDM6, RUNX1, SMAD9, SNAI2, SOX7, SOX9, SP5, SP6, TBX3, TCF21, TFAP2A, TFAP2B, TP63, TWIST1, ZEB2, ZNF436, ZNF750
GO_FOREBRAIN_DEVELOPMENT	5.30E-09	9.86E-07	24	ADGRG1, ALDH1A2, COL3A1, CSF1R, DLC1, DLX1, DLX2, DLX5, DMRTA2, GATA2, ID4, INHBA, ISL1, LEF1, LRP2, MSX1, NOG, NR2F2, PITX1, SLC8A1, TBX3, WNT3A, WNT4, ZEB2
GO_MESONEPHRIC_TUBULE_MORPHOGENESIS	5.33E-09	9.86E-07	11	GATA3, GREB1L, HOXB7, NOG, OSR1, SOX9, TACSTD2, TCF21, WNT4, WNT6, WNT9B
GO_TUBE_FORMATION	6.54E-09	1.19E-06	15	DLC1, FOLR1, GATA3, GRHL3, HAND1, LRP2, NOG, OSR1, SOX9, TGM2, TWIST1, WNT4, WNT6, WNT9B, ZEB2
GO_MESENCHYMAL_CELL_DIFFERENTIATION	6.95E-09	1.24E-06	18	ALDH1A2, EFN1, FOLR1, HEY1, ISL1, LEF1, MSX1, MSX2, NOG, OSR1, SEMA6D, SNAI2, SOX9, TCF21, TWIST1, WNT4, ZEB2, ZNF703
GO_UROGENITAL_SYSTEM_DEVELOPMENT	8.94E-09	1.57E-06	22	ALDH1A2, ANXA1, BMPER, ENPEP, GATA2, GATA3, GREB1L, HOXB7, ID4, MYOCD, NOG, OSR1, SOX9, TACSTD2, TCF21, TFAP2A, TFAP2B, TNC, TP63, WNT4, WNT6, WNT9B
GO_FORELIMB_MORPHOGENESIS	9.23E-09	1.59E-06	9	ALDH1A2, MSX1, MSX2, OSR1, TBX3, TFAP2A, TFAP2B, TP63, TWIST1
GO_MORPHOGENESIS_OF_A_BRANCHING_STRUCTURE	9.42E-09	1.60E-06	17	DLX2, GREB1L, HOXB7, LEF1, MSX2, NOG, SNAI2, SOX9, TACSTD2, TBX3, TCF21, TGM2, TNC, TP63, WNT4, WNT6, WNT9B
GO_POSITIVE_REGULATION_OF_GENE_EXPRESSION	1.08E-08	1.79E-06	63	ACTC1, AFAP1L2, ALDH1A2, BARKX2, CDKN2B, CDX2, DLX1, DLX2, DLX3, DLX5, DLX6, EN2, EPAS1, EVX1, GATA2, GATA3, GDF6, GPER1, GRHL3, HAND1, HEY1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB7, HOXB9, HOXC13, ID4, IL18, INHBA, ISL1, LEF1, LUM, MEIS1, MEIS2, MSX1, MYOCD, NOG, NR2F2, OSR1, PDX1, PITX1, PPARG, PRKD1, RUNX1, SLC40A1, SLC6A4, SMAD9, SOX9, TBX3, TCF21, TFAP2A, TFAP2B, TNC, TP63, TWIST1, WNT3A, WNT4, WNT6, ZEB2, ZNF750, ZNF804A
GO_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	1.23E-08	2.02E-06	59	ACADL, ADRA1B, AFAP1L2, AMOT, ANKRD1, ANXA1, BMPER, CCR1, CD274, CLSTN2, CSF1R, CYP1B1, DIO2, DIO3, DLX1, DLX2, DMRTA2, EPAS1, FGFBP1, FLRT3, GATA2, GATA3, GDF6, GPER1, HOXB7, ID4, IL18, IL1R1, INHBA, ISL1, LEF1, LPL, LRP2, LUM, MSX2, MYOCD, NOG, NPPB, OSR1, P2RY2, PLXNA2, POSTN, PPARG, PRKD1, PRLR, RUNX1, SLC8A1, SOX9, SPHK1, TFAP2A, TP63, TWIST1, VTCN1, WNT3A, WNT4, WNT6, ZEB2, ZNF703, ZNF804A
GO_REGULATION_OF_CELL_DIFFERENTIATION	1.90E-08	3.06E-06	60	ADGRG1, ANKRD1, ANXA1, CCR1, CDX2, CNTN4, COL3A1, DIO3, DLX1, DLX2, DMRTA2, EFN1, GATA2, GATA3, GDF6, GPER1, HEY1, HOXB3, HOXB4, HOXB8, ID4, IGFBP3, IL18, INHBA, ISL1, LEF1, LPL, LRP2, MEIS1, MEIS2, MSX1, MSX2, MYLK3, MYOCD, NOG, OSR1, PLXNA2, POSTN, PPARG, PRDM6, PRKD1, PRTG, RUNX1, SEMA6D, SLC6A4, SNAI2, SOX9, TACSTD2, TBX3, TFAP2A, TFAP2B, TP63, TWIST1, WNT3A, WNT4, WNT5B, WNT9B, ZEB2, ZNF703, ZNF804A
GO_CELL_FATE_COMMITMENT	2.09E-08	3.32E-06	19	DLX1, DLX2, DMRTA2, EPAS1, EVX1, EYA2, GATA2, GATA3, ISL1, NR2F2, PITX1, PPARG, SOX9, TBX3, WNT3A, WNT4, WNT5B, WNT6, WNT9B
GO_CARTILAGE_DEVELOPMENT	2.13E-08	3.33E-06	17	BARKX2, COL11A1, CSGALNACT1, DLX2, GDF6, HAND1, HOXB3, LUM, MSX1, MSX2, NOG, OSR1, PITX1, SNAI2, SOX9, VIT, WNT5B
GO_PROXIMAL_PROMOTER_SEQUENCE_SPECIFIC_DNA_BINDING	2.19E-08	3.35E-06	28	DLX1, DLX2, DLX3, DLX5, DLX6, GATA2, GATA3, HAND1, HOXB2, HOXB3, HOXB7, ISL1, LEF1, MEIS1, MEIS2, MYOCD, PDX1, PITX1, PPARG, RUNX1, SNAI2, SOX9, TBX3, TCF21, TFAP2A, TFAP2B, TWIST1, ZNF750
GO_REGULATION_OF_CELLULAR_COMPONENT_MOVEMENT	2.21E-08	3.35E-06	42	ACKR3, ADGRG1, AMOT, ANXA1, ARHGDI1B, BMPER, CCR1, CD274, COL3A1, CSF1R, CYP1B1, DLC1, EFN1, FGFBP1, GATA2, GATA3, GPER1, IGFBP3, IL1R1, KRT16, LEF1, MYOCD, NOG, NR2F2, P2RY6, PLXNA2, POSTN, PPARG, PRKD1, SEMA6D, SLC8A1, SNAI2, SOX9, SPHK1, TACSTD2, TCAF2, TWIST1, UNC5C, WNT3A, WNT4, WNT5B, ZNF703
GO_EAR_MORPHOGENESIS	2.58E-08	3.82E-06	13	COL11A1, DLX5, DLX6, GATA2, GATA3, GRHL3, MSX1, NOG, OSR1, SOX9, TFAP2A, TWIST1, WNT3A
GO_RENAL_TUBULE_DEVELOPMENT	2.60E-08	3.82E-06	12	GATA3, GREB1L, HOXB7, NOG, OSR1, SOX9, TACSTD2, TCF21, TFAP2B, WNT4, WNT6, WNT9B
GO_EMBRYONIC_FORELIMB_MORPHOGENESIS	2.71E-08	3.87E-06	8	ALDH1A2, MSX1, MSX2, OSR1, TBX3, TFAP2A, TP63, TWIST1
GO_ENDOCARDIAL_CUSHION_MORPHOGENESIS	2.71E-08	3.87E-06	8	HEY1, ISL1, MSX1, MSX2, NOG, SNAI2, SOX9, TWIST1
GO_RESPONSE_TO_GROWTH_FACTOR	2.97E-08	4.18E-06	33	ANKRD1, ANXA1, BMPER, CDKN2B, COL3A1, DLX1, DLX5, FGFBP1, FLRT3, FOLR1, GATA3, GDF6, GREM2, HTRA3, LEF1, LRP2, LUM, MEIS2, MSX1, MSX2, MYOCD, MYOF, NOG, POSTN, PRKD1, SMAD9, SNAI2, SOX9, TFAP2B, TNC, TWIST1, WNT4, ZNF703
GO_POSITIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS	3.13E-08	4.34E-06	62	AFAP1L2, ANKRD1, ANXA1, BARKX2, CDKN2B, CDX2, DLX1, DLX2, DLX3, DLX5, DLX6, EN2, EPAS1, EVX1, GATA2, GATA3, GDF6, GPER1, GRHL3, HAND1, HEY1, HOXB2, HOXB3, HOXB4, HOXB5, HOXB7, HOXB9, HOXC13, ID4, IL18, INHBA, ISL1, LEF1, LUM, MEIS1, MEIS2, MSX1, MYOCD, NOG, NR2F2, OSR1, P2RY6, PDX1, PITX1, PPARG, PRKD1, RUNX1, SLC40A1, SMAD9, SOX9, TBX3, TCF21, TFAP2A, TFAP2B, TP63, TWIST1, VGLL1, WNT3A, WNT4, WNT6, ZEB2, ZNF750
GO_NEPHRON_MORPHOGENESIS	3.18E-08	4.36E-06	11	GATA3, GREB1L, HOXB7, NOG, OSR1, SOX9, TACSTD2, TCF21, WNT4, WNT6, WNT9B
GO_RESPONSE_TO_BMP	4.46E-08	6.03E-06	15	BMPER, DLX1, DLX5, GATA3, GDF6, GREM2, HTRA3, LEF1, LRP2, MSX1, MSX2, NOG, SMAD9, SOX9, TFAP2B
GO_MESONEPHROS_DEVELOPMENT	5.18E-08	6.90E-06	12	BMPER, GATA3, GREB1L, HOXB7, NOG, OSR1, SOX9, TACSTD2, TCF21, WNT4, WNT6, WNT9B
GO_HINDLIMB_MORPHOGENESIS	5.67E-08	7.46E-06	8	MSX1, MSX2, OSR1, PITX1, TBX3, TFAP2B, TP63, TWIST1
GO_REGULATION_OF_DNA_BINDING	5.77E-08	7.50E-06	13	GATA3, HAND1, HEY1, ID4, ISL1, LEF1, MSX1, MSX2, MYOCD, PDX1, PPARG, TWIST1, WNT3A

GO_NEUROGENESIS	6.09E-08	7.81E-06	53	ADGRG1, ALDH1A2, ANKRD1, ANXA1, CNTN4, COL3A1, CSF1R, DIO3, DLX1, DLX2, DLX5, DMRTA2, EFN1, EN2, EVX1, FLRT3, FOLR1, GATA2, GATA3, GDF6, GPER1, HEY1, HOXB3, ID4, INHBA, ISL1, LEF1, LRP2, MAP1A, MEIS1, NOG, NR2F2, PLXNA2, POSTN, PPARG, PRDM6, PRKD1, PRTG, RUNX1, SEMA6D, SH3TC2, SLC6A4, SOX9, TNC, TWIST1, UNC5C, WNT3A, WNT4, WNT5B, WNT6, WNT9B, ZEB2, ZNF804A
GO_CELLULAR_RESPONSE_TO_RETINOIC_ACID	1.06E-07	1.34E-05	10	ALDH1A2, OSR1, PPARG, SLC6A4, SOX9, TNC, WNT3A, WNT5B, WNT6, WNT9B
GO_NEPHRON_EPITHELIUM_DEVELOPMENT	1.09E-07	1.36E-05	12	GATA3, GREB1L, HOXB7, NOG, OSR1, SOX9, TACSTD2, TCF21, TFAP2B, WNT4, WNT6, WNT9B
GO_POSITIVE_REGULATION_OF_CELL_DIFFERENTIATION	1.48E-07	1.82E-05	38	ANKRD1, ANXA1, CCR1, CDX2, DLX1, DLX2, DMRTA2, GATA2, GATA3, GDF6, GPER1, HOXB4, ID4, IGFBP3, IL18, INHBA, ISL1, LEF1, LPL, LRP2, MSX2, MYLK3, MYOCD, PLXNA2, PPARG, PRKD1, RUNX1, SNAI2, SOX9, TACSTD2, TP63, TWIST1, WNT3A, WNT4, WNT5B, ZEB2, ZNF703, ZNF804A
GO_EMBRYONIC_HINDLIMB_MORPHOGENESIS	1.64E-07	2.00E-05	7	MSX1, MSX2, OSR1, PITX1, TBX3, TP63, TWIST1
GO_EPITHELIAL_CELL_PROLIFERATION	1.87E-07	2.23E-05	23	ALDH1A2, BMPER, CDKN2B, DLX5, DLX6, FGFBP1, GATA2, GATA3, IGFBP3, ISL1, NOG, NR2F2, OSR1, PPARG, PRKD1, SNAI2, SOX9, TACSTD2, TGM1, TP63, TWIST1, WNT3A, ZNF703
GO_CONNECTIVE_TISSUE_DEVELOPMENT	1.88E-07	2.23E-05	18	BARX2, COL11A1, CSGALNACT1, DLX2, GDF6, HAND1, HOXB3, ID4, LUM, MSX1, MSX2, NOG, OSR1, PITX1, SNAI2, SOX9, VIT, WNT5B
GO_REGULATION_OF_CELL_POPULATION_PROLIFERATION	2.09E-07	2.45E-05	54	ADGRG1, ALDH1A2, ANXA1, BNC1, CD274, CDKN2B, CDX2, CSF1R, CYP1B1, DLX1, DLX5, DLX6, DMRTA2, FGFBP1, GATA2, GATA3, GPER1, ID4, IGFBP3, IGFBP7, IL18, INHBA, ISL1, LEF1, LRP2, MEIS1, MEIS2, MSX1, MSX2, MYOCD, NOG, NR2F2, OSR1, P2RY6, PDX1, PPARG, PRKD1, SLC6A4, SNAI2, SOX7, SOX9, SPHK1, TACSTD2, TBX3, TFAP2A, TFAP2B, TGM1, TGM2, TNC, TP63, TWIST1, VTCN1, WNT3A, ZNF703
GO_KIDNEY_MORPHOGENESIS	2.22E-07	2.58E-05	11	GATA3, GREB1L, HOXB7, NOG, OSR1, SOX9, TACSTD2, TCF21, WNT4, WNT6, WNT9B
GO_KIDNEY_EPITHELIUM_DEVELOPMENT	2.43E-07	2.79E-05	13	BMPER, GATA3, GREB1L, HOXB7, NOG, OSR1, SOX9, TACSTD2, TCF21, TFAP2B, WNT4, WNT6, WNT9B
GO_ENDOCARDIAL_CUSHION_DEVELOPMENT	2.48E-07	2.81E-05	8	HEY1, ISL1, MSX1, MSX2, NOG, SNAI2, SOX9, TWIST1
GO_NEPHRON_TUBULE_FORMATION	2.79E-07	3.13E-05	6	GATA3, NOG, OSR1, SOX9, WNT6, WNT9B
GO_NEPHRON_DEVELOPMENT	2.87E-07	3.17E-05	13	ENPEP, GATA3, GREB1L, HOXB7, NOG, OSR1, SOX9, TACSTD2, TCF21, TFAP2B, WNT4, WNT6, WNT9B
GO_GLAND_MORPHOGENESIS	2.89E-07	3.17E-05	12	CSF1R, ID4, MSX2, NOG, SNAI2, SOX9, TBX3, TGM2, TNC, TP63, WNT3A, WNT4
GO_POSITIVE_REGULATION_OF_CELL_POPULATION_PROLIFERATION	3.04E-07	3.31E-05	37	ADGRG1, ALDH1A2, ANXA1, BNC1, CD274, CDX2, CSF1R, DLX5, DLX6, DMRTA2, FGFBP1, GATA2, GPER1, ID4, IL18, ISL1, LEF1, LRP2, MEIS2, MYOCD, NOG, OSR1, P2RY6, PDX1, PRKD1, SOX9, SPHK1, TBX3, TFAP2B, TGM1, TGM2, TNC, TP63, TWIST1, VTCN1, WNT3A, ZNF703
GO_REGULATION_OF_ANIMAL_ORGAN_MORPHOGENESIS	3.69E-07	3.96E-05	17	DIO3, GATA3, GRHL3, HOXB7, ISL1, MSX1, NOG, SNAI2, SOX9, SP6, TACSTD2, TFAP2A, TWIST1, WNT3A, WNT4, WNT6, WNT9B
GO_MUSCLE_ORGAN_DEVELOPMENT	3.86E-07	4.10E-05	22	ACTC1, ANKRD1, COL11A1, COL19A1, COL3A1, DMRTA2, HAND1, ISL1, JPH2, LEF1, LRP2, MEIS1, MSX1, MYOCD, NOG, NR2F2, PITX1, POPDC2, SGC, TCF21, TWIST1, WNT3A
GO_SENSORY_ORGAN_MORPHOGENESIS	3.90E-07	4.10E-05	17	COL11A1, DIO3, DLX5, DLX6, GATA2, GATA3, GRHL3, HOXC13, MEIS1, MSX1, NOG, OSR1, SOX9, TFAP2A, TFAP2B, TWIST1, WNT3A
GO_CARDIAC_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	4.42E-07	4.60E-05	7	EFNA1, HEY1, MSX1, MSX2, NOG, SNAI2, TWIST1
GO_NEGATIVE_REGULATION_OF_RNA_BIOSYNTHETIC_PROCESSES	4.50E-07	4.63E-05	43	ANKRD1, BARX2, CDX2, DLX1, DLX2, EFN1, GATA2, GATA3, HAND1, HEY1, HMX1, HOXB3, HOXB4, HOXB8, HR, ID4, ISL1, LEF1, MEIS2, MSX1, MSX2, MYOCD, NOG, NR2F2, OSR1, PDX1, PITX1, PPARG, PRDM6, RUNX1, SNAI2, SOX7, SOX9, SP5, TBX3, TCF21, TFAP2A, TFAP2B, TP63, TWIST1, WNT4, ZEB2, ZNF703
GO_BRANCHING_MORPHOGENESIS_OF_AN_EPITHELIAL_TUBE	5.41E-07	5.52E-05	13	GREB1L, HOXB7, LEF1, MSX2, NOG, SOX9, TACSTD2, TBX3, TCF21, TNC, WNT4, WNT6, WNT9B
GO_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	6.09E-07	6.15E-05	16	ACTC1, ALDH1A2, ANKRD1, COL11A1, HAND1, ISL1, JPH2, LRP2, MEIS1, MYLK3, MYOCD, NOG, SGC, SLC8A1, TBX3, WNT3A
GO_RESPONSE_TO_RETINOIC_ACID	6.80E-07	6.80E-05	11	ALDH1A2, IGFBP7, OSR1, PPARG, SLC6A4, SOX9, TNC, WNT3A, WNT5B, WNT6, WNT9B
GO_ENDOCRINE_SYSTEM_DEVELOPMENT	6.95E-07	6.88E-05	12	ALDH1A2, ANXA1, GATA2, GATA3, HOXB3, ISL1, MSX1, NOG, PDX1, PITX1, SOX9, WNT4
GO_SENSORY_SYSTEM_DEVELOPMENT	8.06E-07	7.89E-05	20	ADAMTS18, ALDH1A2, CYP1B1, DIO3, DLX1, DLX2, GATA3, GRHL3, INHBA, ISL1, MEIS1, MEIS2, SOX9, TFAP2A, TFAP2B, TWIST1, WNT5B, WNT6, WNT9B, ZEB2
GO_ODONTOGENESIS_OF_DENTIN_CONTAINING_TOOTH	9.46E-07	9.18E-05	10	DLX1, DLX2, DLX3, HAND1, LEF1, MSX1, MSX2, TNC, TP63, WNT6
GO_CELLULAR_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	9.91E-07	9.52E-05	25	ANKRD1, ANXA1, CASQ2, COLEC12, CYP1B1, FOLR1, GPER1, IL18, INHBA, ISL1, LEF1, MSX2, NR2F2, P2RY2, P2RY6, PPARG, RUNX1, SLC6A4, SLC8A1, SNAI2, SP5, TCF21, TNC, TP63, ZNF703
GO_CELLULAR_RESPONSE_TO_ENDOGENOUS_STIMULUS	1.21E-06	1.15E-04	45	ANKRD1, ANXA1, BMPER, CASQ2, CDKN2B, COL3A1, DLX1, DLX5, FGFBP1, FLRT3, FOLR1, GATA3, GDF6, GPER1, GREM2, HTRA3, IGFBP7, INHBA, ISL1, LEF1, LPL, LRP2, LYPD1, MSX1, MSX2, MYOCD, NOG, NR2F2, P2RY2, P2RY6, POSTN, PPARG, PRLR, RUNX1, SLC6A4, SLC8A1, SMAD9, SNAI2, SOX9, TCF21, TFAP2B, TNC, TP63, WNT4, ZNF703
GO_CELL_MOTILITY	1.40E-06	1.32E-04	52	ACKR3, ADGRG1, AMOT, ANXA1, ARHGDI1B, BMPER, CCR1, CD274, COL3A1, CSF1R, CYP1B1, DLX1, EFN1, ENPEP, FGFBP1, FLRT3, FOLR1, GATA2, GATA3, GPER1, HOXB9, IGFBP3, IL1R1, ISL1, ITGB6, KRT16, LCP1, LEF1, MSX2, MYOCD, NOG, NR2F2, P2RY6, PIK3C2G, PLXNA2, POSTN, PPARG, PRKD1, PSTPIP2, SEMA6D, SLC8A1, SNAI2, SOX9, SPHK1, TACSTD2, TCAFA2, TWIST1, UNC5C, WNT4, WNT5B, ZEB2, ZNF703
GO_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	1.55E-06	1.44E-04	12	EFNA1, HEY1, ISL1, LEF1, MSX1, MSX2, NOG, SNAI2, SOX9, TWIST1, WNT4, ZNF703
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	1.82E-06	1.68E-04	19	BMPER, CDKN2B, COL3A1, DLX1, DLX5, FOLR1, GDF6, GREM2, HTRA3, INHBA, LEF1, LRP2, MSX1, MSX2, MYOCD, NOG, SMAD9, TFAP2B, ZNF703
GO_MAMMARY_GLAND_DEVELOPMENT	1.94E-06	1.78E-04	12	CSF1R, GATA3, HOXB9, LEF1, MSX1, MSX2, PRLR, SOX9, TBX3, WNT3A, WNT4, ZNF703
GO_OSSIFICATION	2.17E-06	1.97E-04	20	CCR1, COL11A1, CSGALNACT1, DLX5, ID4, IGFBP3, LEF1, MSX2, NOG, OSR1, PRKD1, SLC8A1, SNAI2, SOX9, TFAP2A, TNC, TP63, TWIST1, WNT3A, WNT4
GO_REGULATION_OF_KIDNEY_DEVELOPMENT	2.34E-06	2.11E-04	8	GATA3, HOXB7, NOG, OSR1, SOX9, TACSTD2, WNT4, WNT9B
GO_NEGATIVE_REGULATION_OF_CELL_POPULATION_PROLIFERATION	2.42E-06	2.15E-04	30	ADGRG1, ALDH1A2, CD274, CDKN2B, CSF1R, CYP1B1, DLX1, FGFBP1, GATA2, GATA3, GPER1, IGFBP3, IGFBP7, INHBA, ISL1, MEIS1, MSX1, MSX2, MYOCD, NOG, NR2F2, PDX1, PPARG, SLC6A4, SNAI2, SOX7, SOX9, TFAP2A, TFAP2B, VTCN1
GO_CELLULAR_RESPONSE_TO_LIPID	2.44E-06	2.15E-04	26	ALDH1A2, ANKRD1, ANXA1, CD274, GPER1, IL18, INHBA, ISL1, LEF1, MSX2, NR2F2, OSR1, P2RY6, PPARG, RUNX1, SLC6A4, SNAI2, SOX9, TCF21, TNC, TP63, WNT3A, WNT5B, WNT6, WNT9B, ZNF703
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	2.45E-06	2.15E-04	17	BMPER, CDKN2B, DLX1, FGFBP1, FOLR1, GATA3, GREM2, HTRA3, LRP2, MSX1, MSX2, MYOCD, MYOF, NOG, TFAP2B, WNT4, ZNF703
GO_EPITHELIAL_CELL_DIFFERENTIATION	2.55E-06	2.22E-04	30	ANXA1, CDX2, DLX3, DLX5, DLX6, GATA3, HEY1, HOXB5, KRT16, KRT17, KRT23, KRT80, LEF1, MSX2, NR2F2, OSR1, PDX1, PPARG, RUNX1, SOX9, TBX3, TCF21, TGM1, TP63, UPK2, WNT4, WNT5B, WNT9B, ZEB2, ZNF703

GO_REGULATION_OF_ANATOMICAL_STRUCTURE_MORPHOGENESIS	2.67E-06	2.29E-04	39	AMOT, ANXA1, BMPER, CDX2, CSF1R, CYP1B1, DIO3, DLX1, EFN1, FGFBP1, GATA2, GATA3, GRHL3, HEY1, HOXB7, ISL1, MSX1, MYLK3, NOG, NPPB, OSR1, PLXNA2, POSTN, PPARG, PRKD1, RUNX1, SEMA6D, SNAI2, SOX9, SP6, SPHK1, TACSTD2, TFAP2A, TWIST1, WNT3A, WNT4, WNT6, WNT9B, ZEB2
GO_NEGATIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	2.68E-06	2.29E-04	42	ADAMTS18, ADGRG1, AMOT, ANXA1, ARHGDIB, CCR1, CD274, CNTN4, COL3A1, DIO3, DLX1, DLX2, EFN1, GATA2, GATA3, GUCY1A1, HOXB8, ID4, INHBA, ISL1, LEF1, MEIS1, MEIS2, MSX2, MYOCD, NOG, NPPB, NR2F2, OSR1, PPARG, PRTG, RUNX1, SEMA6D, SLC6A4, SNAI2, SOX9, TACSTD2, TP63, TWIST1, WNT3A, WNT4, WNT9B
GO_RENAL_SYSTEM_DEVELOPMENT	3.09E-06	2.62E-04	17	ALDH1A2, BMPER, ENPEP, GATA3, GREB1L, HOXB7, MYOCD, NOG, OSR1, SOX9, TACSTD2, TCF21, TFAP2A, TFAP2B, WNT4, WNT6, WNT9B
GO_NEGATIVE_REGULATION_OF_PHOTORECEPTOR_CELL_DIFFERENTIATION	3.57E-06	3.00E-04	4	DIO3, DLX1, DLX2, SOX9
GO_PITUITARY_GLAND_DEVELOPMENT	3.66E-06	3.05E-04	7	ALDH1A2, GATA2, ISL1, MSX1, NOG, PITX1, WNT4
GO_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	3.98E-06	3.28E-04	15	BMPER, CDKN2B, DLX1, FOLR1, GDF6, GREM2, HTRA3, INHBA, LRP2, MSX1, MSX2, MYOCD, NOG, TFAP2B, ZNF703
GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_CELL_FATE_COMMITMENT	4.30E-06	3.52E-04	5	DLX1, DLX2, EVX1, NR2F2, PPARG
GO_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	4.37E-06	3.55E-04	33	ADGRG1, ANKRD1, CLSTN2, CNTN4, COL3A1, DIO3, DLX1, DLX2, DMRTA2, EFN1, FLRT3, GATA2, GATA3, GDF6, GPER1, GRHL3, HEY1, HOXB3, ID4, ISL1, LRP2, MEIS1, NOG, PLXNA2, PPARG, PRKD1, PRTG, SEMA6D, SLC6A4, SOX9, WNT3A, ZEB2, ZNF804A
GO_NEGATIVE_REGULATION_OF_CELL_DEVELOPMENT	4.43E-06	3.57E-04	18	ADGRG1, CNTN4, COL3A1, DIO3, DLX1, DLX2, EFN1, ID4, ISL1, MEIS1, NOG, POSTN, PRTG, SEMA6D, SLC6A4, SOX9, TACSTD2, WNT3A
GO_POSITIVE_REGULATION_OF_ANIMAL_ORGAN_MORPHOGENESIS	4.46E-06	3.57E-04	9	GATA3, HOXB7, NOG, SOX9, TFAP2A, TWIST1, WNT3A, WNT4, WNT6
GO_CAMERA_TYPE_EYE_DEVELOPMENT	4.83E-06	3.83E-04	17	ALDH1A2, CYP1B1, DIO3, DLX1, DLX2, GATA3, GRHL3, INHBA, MEIS1, SOX9, TFAP2A, TFAP2B, TWIST1, WNT5B, WNT6, WNT9B, ZEB2
GO_LOCOMOTION	4.97E-06	3.91E-04	55	ACKR3, ADGRG1, AMOT, ANXA1, ARHGDIB, BMPER, CCR1, CD274, CNTN4, COL3A1, CSF1R, CYP1B1, DLX1, DLX5, EFN1, ENPEP, FGFBP1, FLRT3, FOLR1, GATA2, GATA3, GPER1, HOXB9, IGFBP3, IL1R1, ISL1, ITGB6, KRT16, LCP1, LEF1, MSX2, MYOCD, NOG, NR2F2, P2RY6, PIK3C2G, PLXNA2, POSTN, PPARG, PRKD1, PSTPIP2, SEMA6D, SLC8A1, SNAI2, SOX9, SPHK1, TACSTD2, TCAF2, TWIST1, UNC5C, WNT3A, WNT4, WNT5B, ZEB2, ZNF703
GO_EAR_DEVELOPMENT	6.03E-06	4.71E-04	14	BMPER, COL11A1, DLX5, DLX6, GATA2, GATA3, GRHL3, MSX1, NOG, OSR1, SOX9, TFAP2A, TWIST1, WNT3A
GO_MESONEPHRIC_TUBULE_FORMATION	6.36E-06	4.93E-04	4	GATA3, NOG, OSR1, WNT9B
GO_ENHANCER_BINDING	6.41E-06	4.93E-04	11	CDX2, GATA2, GATA3, HOXB5, HOXB6, HOXB7, ISL1, LEF1, MSX1, SOX9, TFAP2B
GO_FOREBRAIN_GENERATION_OF_NEURONS	7.24E-06	5.52E-04	8	CSF1R, DLX1, DLX2, DLX5, GATA2, INHBA, LEF1, WNT3A
GO_REGULATION_OF_CELL_DEVELOPMENT	7.69E-06	5.82E-04	33	ADGRG1, ANKRD1, CNTN4, COL3A1, DIO3, DLX1, DLX2, DMRTA2, EFN1, GATA2, GATA3, GDF6, GPER1, HEY1, HOXB3, ID4, ISL1, LRP2, MEIS1, MYLK3, NOG, PLXNA2, POSTN, PPARG, PRKD1, PRTG, SEMA6D, SLC6A4, SOX9, TACSTD2, WNT3A, ZEB2, ZNF804A
GO_REGULATION_OF_BMP_SIGNALING_PATHWAY	8.03E-06	6.04E-04	9	BMPER, DLX1, GREM2, HTRA3, LRP2, MSX1, MSX2, NOG, TFAP2B
GO_AMEBOIDAL_TYPE_CELL_MIGRATION	9.31E-06	6.95E-04	21	AMOT, ANXA1, ARHGDIB, BMPER, CYP1B1, EFN1, FGFBP1, FOLR1, GATA2, GATA3, ISL1, KRT16, NR2F2, PPARG, PRKD1, SEMA6D, SLC8A1, SOX9, TACSTD2, TWIST1, ZEB2
GO_REGULATION_OF_OSSIFICATION	9.53E-06	7.06E-04	13	CCR1, ID4, MSX2, NOG, OSR1, PRKD1, SLC8A1, SNAI2, SOX9, TFAP2A, TP63, TWIST1, WNT4
GO_CELL_CELL_SIGNALING	9.93E-06	7.30E-04	48	ADGRG1, ADRA1B, AMER2, ANXA1, CACNG4, CASQ2, CCR1, CLSTN2, CNTN4, DKK2, DLX5, EFN1, ENPEP, FGFBP1, FOLR1, GATA3, GJD2, GPER1, GRHL3, GUCY1A1, IL18, INHBA, ISL1, LEF1, LYPD1, MAP1A, NOG, NPBBWR1, PDX1, RUNX1, SIGLEC6, SLC6A4, SNAI2, SOX7, SOX9, STC2, TBX3, TFAP2B, TNC, TP63, WLS, WNT3A, WNT4, WNT5B, WNT6, WNT9B, ZEB2, ZNF703
GO_REGULATION_OF_PHOTORECEPTOR_CELL_DIFFERENTIATION	1.05E-05	7.64E-04	4	DIO3, DLX1, DLX2, SOX9
GO_RESPONSE_TO_ENDOGENOUS_STIMULUS	1.06E-05	7.67E-04	48	ALDH1A2, ANKRD1, ANXA1, BMPER, CASQ2, CDKN2B, COL3A1, DLX1, DLX5, FGFBP1, FLRT3, FOLR1, GATA3, GDF6, GPER1, GREM2, HTRA3, IGFBP7, INHBA, ISL1, LEF1, LPL, LRP2, LYPD1, MSX1, MSX2, MYOCD, NOG, NR2F2, P2RY2, P2RY6, PAPP, PDX1, POSTN, PPARG, PRLR, RUNX1, SLC6A4, SLC8A1, SMAD9, SNAI2, SOX9, TCF21, TFAP2B, TNC, TP63, WNT4, ZNF703
GO_ENZYME_LINKED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	1.08E-05	7.80E-04	35	AFAP1L2, BMPER, CDKN2B, COL3A1, CSF1R, DLX1, DLX5, EFN1, FGFBP1, FLRT3, FOLR1, GATA3, GDF6, GPER1, GPRC5A, GREM2, HTRA3, IGFBP3, INHBA, LEF1, LRP2, MSX1, MSX2, MYOCD, MYOF, NOG, NPPB, PRKD1, PRLR, SH3TC2, SMAD9, SOX9, TFAP2B, WNT4, ZNF703
GO_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	1.23E-05	8.77E-04	32	ALDH1A2, ANKRD1, ANXA1, CACNG4, CASQ2, COLEC12, CYP1B1, FOLR1, GPER1, IGFBP7, IL18, INHBA, ISL1, LEF1, LUM, MSX2, NR2F2, P2RY2, P2RY6, PAPP, PDX1, POSTN, PPARG, RUNX1, SLC6A4, SLC8A1, SNAI2, SP5, TCF21, TNC, TP63, ZNF703
GO_REGULATION_OF_TRANSCRIPTION_REGULATORY_REGION_DNA_BINDING	1.35E-05	9.58E-04	7	GATA3, HAND1, HEY1, MSX1, MSX2, TWIST1, WNT3A
GO_CANONICAL_WNT_SIGNALING_PATHWAY	1.36E-05	9.59E-04	17	AMER2, DKK2, DLX5, FOLR1, GATA3, ISL1, LEF1, NOG, SNAI2, SOX7, SOX9, WLS, WNT3A, WNT4, WNT5B, WNT9B, ZNF703
GO_DEVELOPMENTAL_PROCESS_INVOLVED_IN_REPRODUCTION	1.48E-05	1.04E-03	26	ADGRG1, ANXA1, CDX2, DLX3, EPAS1, GATA2, GATA3, GREB1L, HAND1, HEY1, ID4, INHBA, LEF1, LRP2, MYOCD, NOG, NR2F2, OSR1, PPARG, SOX9, TBX3, TCF21, TNC, TP63, WNT4, WNT9B
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	1.55E-05	1.08E-03	13	DLX5, DLX6, FGFBP1, GATA2, NOG, OSR1, PRKD1, SOX9, TGM1, TP63, TWIST1, WNT3A, ZNF703
GO_FORMATION_OF_PRIMARY_GERM_LAYER	1.58E-05	1.09E-03	10	COL11A1, EYA2, HAND1, INHBA, LAMB3, LEF1, NOG, SOX7, WLS, WNT3A
GO_REGULATION_OF_CELL_DEATH	1.59E-05	1.09E-03	49	ACKR3, ACTC1, ADCY10, ALDH1A2, ANKRD1, ANXA1, CD274, CSF1R, CYP1B1, DLX1, DLX5, EFN1, EN2, EYA2, GATA2, GATA3, GDF6, GPER1, IGFBP3, INHBA, ISL1, LEF1, MAL, MSX1, MSX2, MYOCD, NOG, OSR1, PDX1, PPARG, PRKD1, PRLR, SLC40A1, SNAI2, SOX7, SOX9, SPHK1, TBX3, TCIM, TFAP2A, TFAP2B, TGM2, TNFSF15, TP63, TWIST1, UNC5C, VTCN1, WNT3A, WNT4
GO_SEMI_LUNAR_VALVE_DEVELOPMENT	1.61E-05	1.09E-03	6	EFN1, GATA3, HEY1, SNAI2, SOX9, TWIST1
GO_INNER_EAR_MORPHOGENESIS	1.64E-05	1.11E-03	9	COL11A1, DLX5, DLX6, GATA2, GATA3, GRHL3, SOX9, TFAP2A, WNT3A
GO_CELLULAR_RESPONSE_TO_ACID_CHEMICAL	1.81E-05	1.22E-03	13	ALDH1A2, COL3A1, FOLR1, OSR1, P2RY6, PPARG, SLC6A4, SOX9, TNC, WNT3A, WNT5B, WNT6, WNT9B
GO_MESODERM_MORPHOGENESIS	2.08E-05	1.39E-03	8	EYA2, HAND1, INHBA, LEF1, NOG, TBX3, WLS, WNT3A
GO_NEGATIVE_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	2.12E-05	1.40E-03	16	ADGRG1, CNTN4, COL3A1, DIO3, DLX1, DLX2, EFN1, ID4, ISL1, MEIS1, NOG, PRTG, SEMA6D, SLC6A4, SOX9, WNT3A
GO_MUSCLE_CELL_DIFFERENTIATION	2.28E-05	1.50E-03	18	ACTC1, ANKRD1, BARX2, CASQ2, GPER1, HEY1, LMOD2, MSX1, MYLK3, MYOCD, MYOF, POPDC2, PRDM6, SLC8A1, SOX9, TBX3, WNT3A, WNT4
GO_DIENCEPHALON_DEVELOPMENT	2.29E-05	1.50E-03	8	ALDH1A2, GATA2, ISL1, MSX1, NOG, PITX1, WNT4, ZEB2

GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DIFFERENTIATION	2.34E-05	1.52E-03	12	CSF1R, DLX1, DLX2, DLX5, EVX1, GATA2, ID4, INHBA, ISL1, WNT3A, WNT9B, ZEB2
GO_HINDBRAIN_DEVELOPMENT	2.42E-05	1.55E-03	11	ALDH1A2, DLX1, EN2, GATA2, HOXB2, HOXB3, LEF1, NOG, PLXNA2, SLC6A4, WLS
GO_CARDIAC_VENTRICLE_DEVELOPMENT	2.42E-05	1.55E-03	10	COL11A1, GATA3, GREB1L, HAND1, HEY1, ISL1, LRP2, MYOCD, NOG, TBX3
GO_GASTRULATION	2.47E-05	1.57E-03	12	AMOT, COL11A1, EYA2, HAND1, INHBA, LAMB3, LEF1, NOG, OSR1, SOX7, WLS, WNT3A
GO_OSTEOBLAST_DIFFERENTIATION	2.71E-05	1.71E-03	13	DLX3, ID4, IGFBP3, LEF1, MSX2, NOG, PRKD1, SNAI2, TNC, TP63, TWIST1, WNT3A, WNT4
GO_BIOLOGICAL_ADHESION	2.72E-05	1.71E-03	42	ACKR3, ADAMTS18, ADGRG1, ANXA1, ARHGDIB, CCR1, CD274, CDH10, CLSTN2, CNTN4, COL19A1, COL3A1, COL6A6, CSRP1, CYP1B1, DLX1, EFN1, FLRT3, GATA3, HAPLN1, IGFBP7, IL18, ITGB6, LAMB3, LEF1, NECTIN4, PLXNA2, POSTN, RUNX1, SERPINB8, SIGLEC6, SNAI2, SOX9, SVEP1, TACSTD2, TGM2, TNC, VIT, VTCN1, WNT3A, WNT4, ZNF703
GO_CHROMATIN_BINDING	3.02E-05	1.88E-03	22	BARX2, DLX1, DLX2, DLX3, GATA2, GPER1, GRHL3, HOXC13, HR, ISL1, LEF1, MEIS1, PDX1, PPARG, PRDM6, SNAI2, SOX9, SVEP1, TFAP2A, TFAP2B, TP63, ZNF750
GO_POSITIVE_REGULATION_OF_LOCOMOTION	3.21E-05	1.99E-03	23	ACKR3, ANXA1, CCR1, CD274, CSF1R, FGFBP1, GATA2, GATA3, GPER1, IL1R1, LEF1, P2RY6, POSTN, PRKD1, SEMA6D, SLC8A1, SNAI2, SOX9, SPHK1, TCAF2, TWIST1, WNT5B, ZNF703
GO_RESPONSE_TO_LIPID	3.38E-05	2.09E-03	31	ALDH1A2, ANKRD1, ANXA1, CD274, GATA2, GPER1, IGFBP7, IL18, INHBA, ISL1, LEF1, MSX2, NR2F2, OSR1, P2RY6, PAPP4, PDX1, POSTN, PPARG, RUNX1, SLC6A4, SNAI2, SOX9, TCF21, TNC, TP63, WNT3A, WNT5B, WNT6, WNT9B, ZNF703
GO_EYELID_DEVELOPMENT_IN_CAMERA_TYPE_EYE	3.44E-05	2.09E-03	4	GRHL3, INHBA, TFAP2A, TWIST1
GO_HEART_VALVE_FORMATION	3.44E-05	2.09E-03	4	EFNA1, HEY1, SOX9, TWIST1
GO_METANEPHRIC_MESENCHYMAL_CELL_DIFFERENTIATION	3.46E-05	2.10E-03	3	OSR1, TCF21, WNT4
GO_METANEPHRIC_NEPHRON_DEVELOPMENT	3.48E-05	2.10E-03	6	OSR1, SOX9, TCF21, TFAP2B, WNT4, WNT9B
GO_NEGATIVE_REGULATION_OF_BIOSYNTHETIC_PROCESS	3.71E-05	2.22E-03	46	ACADL, ANKRD1, BARX2, CDX2, DLX1, DLX2, EFN1, GATA2, GATA3, GPER1, HAND1, HEY1, HMX1, HOXB3, HOXB4, HOXB8, HR, ID4, INHBA, ISL1, LEF1, MEIS2, MSX1, MYOCD, NOG, NR2F2, OSR1, PDX1, PITX1, PPARG, PRDM6, RUNX1, SNAI2, SOX7, SOX9, SP5, TBX3, TCF21, TFAP2A, TFAP2B, TP63, TWIST1, WNT4, ZEB2, ZNF703
GO_MESODERM_DEVELOPMENT	3.87E-05	2.30E-03	10	EYA2, HAND1, INHBA, LEF1, NOG, OSR1, TBX3, TP63, WLS, WNT3A
GO_POSITIVE_REGULATION_OF_DNA_BINDING	3.92E-05	2.32E-03	7	GATA3, ISL1, MYOCD, PDX1, PPARG, TWIST1, WNT3A
GO_PHARYNGEAL_SYSTEM_DEVELOPMENT	4.09E-05	2.39E-03	5	FOLR1, GATA3, ISL1, NOG, PLXNA2
GO_REGULATION_OF_MESONEPHROS_DEVELOPMENT	4.09E-05	2.39E-03	5	GATA3, HOXB7, NOG, SOX9, TACSTD2
GO_NEURON_DIFFERENTIATION	4.21E-05	2.45E-03	40	ALDH1A2, ANKRD1, CNTN4, CSF1R, DIO3, DLX1, DLX2, DLX3, DMRTA2, EFN1, EN2, EVX1, FLRT3, FOLR1, GATA2, GATA3, GDF6, ID4, INHBA, ISL1, LRP2, MAP1A, MEIS1, NOG, PLXNA2, POSTN, PRKD1, RUNX1, SEMA6D, SLC6A4, SOX9, TNC, UNC5C, WNT3A, WNT4, WNT5B, WNT6, WNT9B, ZEB2, ZNF804A
GO_MYOBlast_DIFFERENTIATION	4.33E-05	2.50E-03	8	EPAS1, IGFBP3, IL18, ISL1, MYOCD, PITX1, SOX9, TBX3
GO_GABAERGIC_NEURON_DIFFERENTIATION	4.75E-05	2.71E-03	4	DLX1, DLX2, GATA2, INHBA
GO_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_INVOLVED_IN_HEART_DEVELOPMENT	4.75E-05	2.71E-03	4	MSX1, MSX2, MYOCD, NOG
GO_CELL_CELL_SIGNALING_BY_WNT	4.77E-05	2.71E-03	21	AMER2, DKK2, DLX3, FOLR1, GATA3, GRHL3, ISL1, LEF1, NOG, RUNX1, SNAI2, SOX7, SOX9, WLS, WNT3A, WNT4, WNT5B, WNT6, WNT9B, ZEB2, ZNF703
GO_POSITIVE_REGULATION_OF_OSSIFICATION	5.13E-05	2.90E-03	8	ID4, MSX2, OSR1, PRKD1, SLC8A1, TFAP2A, TP63, WNT4
GO_CARDIAC_CHAMBER_DEVELOPMENT	5.42E-05	3.04E-03	11	COL11A1, GATA3, GREB1L, HAND1, HEY1, ISL1, LRP2, MSX2, MYOCD, NOG, TBX3
GO_BONE_MORPHOGENESIS	5.61E-05	3.13E-03	9	CSGALNACT1, DLX3, MSX1, MSX2, SOX9, SP5, TFAP2A, TWIST1, VIT
GO_AORTIC_VALVE_DEVELOPMENT	5.95E-05	3.26E-03	5	EFNA1, GATA3, SNAI2, SOX9, TWIST1
GO_BHLH_TRANSCRIPTION_FACTOR_BINDING	5.95E-05	3.26E-03	5	HAND1, ISL1, SOX9, TCF21, TWIST1
GO_PROSTATE_GLAND_MORPHOGENESIS	5.95E-05	3.26E-03	5	ID4, NOG, SOX9, TNC, TP63
GO_DNA_BINDING_TRANSCRIPTION_REPRESSOR_ACTIVITY_RNA_POLYMERASE_II_SPECIFIC	5.97E-05	3.26E-03	13	CDX2, GATA3, HAND1, HEY1, HMX1, MSX1, MSX2, PPARG, SNAI2, TBX3, TCF21, TFAP2A, ZEB2
GO_MUSCLE_ORGAN_MORPHOGENESIS	6.06E-05	3.27E-03	8	ACTC1, ANKRD1, COL11A1, COL3A1, HAND1, ISL1, LRP2, NOG
GO_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	6.06E-05	3.27E-03	8	CCR1, OSR1, SLC8A1, SOX9, TFAP2A, TWIST1, WNT4, WNT6
GO_NEURAL_CRESCENT_CELL_DIFFERENTIATION	6.57E-05	3.53E-03	8	ALDH1A2, FOLR1, ISL1, SEMA6D, SNAI2, SOX9, TWIST1, ZEB2
GO_BMP_SIGNALING_PATHWAY_INVOLVED_IN_HEART_DEVELOPMENT	6.84E-05	3.64E-03	3	MSX1, MSX2, NOG
GO_METANEPHRIC_TUBULE_FORMATION	6.84E-05	3.64E-03	3	SOX9, WNT4, WNT9B
GO_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_IN_HEART_DEVELOPMENT	7.10E-05	3.74E-03	5	HEY1, MSX1, MSX2, NOG, WNT3A
GO_METANEPHROS_DEVELOPMENT	7.12E-05	3.74E-03	8	GATA3, GREB1L, OSR1, SOX9, TCF21, TFAP2B, WNT4, WNT9B
GO_PROSTATE_GLAND_DEVELOPMENT	7.70E-05	4.03E-03	6	ANXA1, ID4, NOG, SOX9, TNC, TP63
GO_SOMITE_DEVELOPMENT	8.32E-05	4.32E-03	8	ALDH1A2, CDX2, LEF1, NOG, PLXNA2, WNT3A, WNT4, ZEB2
GO_EPITHELIAL_TO_MESENCHYMAL_TRANSITION_INVOLVED_IN_ENDOCARDIAL_CUSHION_FORMATION	8.44E-05	4.32E-03	4	MSX1, MSX2, NOG, SNAI2
GO_NEPHRIC_DUCT_DEVELOPMENT	8.44E-05	4.32E-03	4	GATA3, GREB1L, OSR1, WNT9B
GO_URETER_DEVELOPMENT	8.44E-05	4.32E-03	4	ALDH1A2, GATA3, OSR1, SOX9
GO_CARDIAC_MUSCLE_TISSUE_MORPHOGENESIS	8.73E-05	4.45E-03	7	ACTC1, ANKRD1, COL11A1, HAND1, ISL1, LRP2, NOG
GO_IN_UTERO_EMBRYONIC_DEVELOPMENT	8.86E-05	4.50E-03	16	AMOT, CDX2, EPAS1, GATA2, GATA3, HAND1, HEY1, LEF1, MSX1, NOG, NR2F2, PLPP4, TBX3, TWIST1, WNT3A, WNT9B
GO_NEGATIVE_REGULATION_OF_CELL_DEATH	9.37E-05	4.73E-03	32	ACKR3, ACTC1, ANXA1, CSF1R, DLX1, EFN1, EN2, EYA2, GATA2, GATA3, ISL1, LEF1, MSX1, MSX2, MYOCD, NOG, OSR1, PDX1, PRKD1, PRLR, SLC40A1, SNAI2, SOX9, SPHK1, TBX3, TCIM, TFAP2A, TFAP2B, TWIST1, VTCN1, WNT3A, WNT4
GO_CELLULAR_RESPONSE_TO_NUTRIENT	9.58E-05	4.81E-03	7	CDKN2B, FOLR1, P2RY2, POSTN, PPARG, SNAI2, TNC
GO_NEGATIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	9.78E-05	4.89E-03	6	GATA2, GATA3, GPER1, ID4, MSX2, WNT3A
GO_MAMMARY_GLAND_EPITHELIUM_DEVELOPMENT	1.05E-04	5.19E-03	7	CSF1R, GATA3, MSX1, MSX2, TBX3, WNT4, ZNF703
GO_REGULATION_OF_BONE_MINERALIZATION	1.05E-04	5.19E-03	7	CCR1, OSR1, SLC8A1, SOX9, TFAP2A, TWIST1, WNT4
GO_REGULATION_OF_VASCULATURE_DEVELOPMENT	1.07E-04	5.25E-03	18	AMOT, ANXA1, BMPER, CYP1B1, EFN1, FGFBP1, GATA2, GPER1, HEY1, ISL1, MYOCD, NPPB, PPARG, PRKD1, RUNX1, SPHK1, TWIST1, WNT4
GO_FACE_DEVELOPMENT	1.10E-04	5.38E-03	6	ALDH1A2, DLX3, HOXB3, LEF1, MSX1, NOG
GO_CARDIAC_VENTRICLE_MORPHOGENESIS	1.15E-04	5.59E-03	7	COL11A1, GATA3, HAND1, HEY1, ISL1, LRP2, NOG
GO_CELLULAR_RESPONSE_TO_VITAMIN	1.16E-04	5.60E-03	5	FOLR1, POSTN, PPARG, SNAI2, TNC
GO_PROXIMAL_DISTAL_PATTERN_FORMATION	1.16E-04	5.60E-03	5	ALDH1A2, DLX1, DLX2, OSR1, TP63
GO_NEGATIVE_REGULATION_OF_CELL_ADHESION	1.20E-04	5.77E-03	14	ADAMTS18, ANXA1, ARHGDIB, CD274, CYP1B1, DLX1, PLXNA2, POSTN, RUNX1, SNAI2, TACSTD2, TNC, VTCN1, ZNF703
GO_NEGATIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	1.23E-04	5.87E-03	6	BMPER, DLX1, GREM2, HTRA3, LRP2, NOG
GO_REGULATION_OF_WNT_SIGNALING_PATHWAY	1.23E-04	5.87E-03	16	AMER2, DKK2, DLX3, FOLR1, ISL1, LEF1, NOG, RUNX1, SNAI2, SOX7, SOX9, WLS, WNT3A, WNT5B, ZEB2, ZNF703
GO_ARTERY_MORPHOGENESIS	1.25E-04	5.93E-03	7	COL3A1, FOLR1, HEY1, LRP2, MYOCD, NOG, TFAP2B
GO_TISSUE_MIGRATION	1.32E-04	6.21E-03	16	ACTC1, AMOT, ANXA1, BMPER, CYP1B1, EFN1, FGFBP1, GATA2, GATA3, KRT16, NR2F2, PPARG, PRKD1, SOX9, TACSTD2, ZEB2
GO_TELENCEPHALON_DEVELOPMENT	1.38E-04	6.46E-03	13	ADGRG1, COL3A1, CSF1R, DLX1, DLX2, DLX3, DMRTA2, ID4, INHBA, LEF1, SLC8A1, WNT3A, ZEB2

GO_APOPTOTIC_PROCESS	1.38E-04	6.46E-03	51	ACKR3, ACTC1, ADCY10, ALDH1A2, ANKRD1, ANXA1, CD274, CSF1R, CYP1B1, DIO3, DLX1, DLX1, EFN1, EN2, EYA2, GATA2, GATA3, GDF6, GPER1, IGFBP3, INHBA, ISL1, LEF1, MAL, MSX1, MSX2, MYOCD, NOG, OSR1, PDX1, PPARG, PRKD1, PRLR, SLC40A1, SNAI2, SOX7, SOX9, SPHK1, TBX3, TCIM, TFAP2A, TFAP2B, TGM2, TNFRSF19, TNFSF15, TP63, TWIST1, UNC5C, VTCN1, WNT3A, WNT4
GO_REGULATION_OF_CELL_ADHESION	1.45E-04	6.75E-03	24	ADAMTS18, ADGRG1, ANXA1, ARHGDIB, CD274, CYP1B1, DLX1, EFN1, GATA3, IL18, LEF1, PLXNA2, POSTN, RUNX1, SNAI2, SOX9, TACSTD2, TGM2, TNC, VIT, VTCN1, WNT3A, WNT4, ZNF703
GO_FAT_CELL_DIFFERENTIATION	1.47E-04	6.80E-03	12	GATA2, GATA3, GDF6, GPER1, ID4, LAMB3, MSX2, PPARG, SNAI2, TFAP2B, WNT3A, WNT5B
GO_NEGATIVE_REGULATION_OF_DNA_BINDING	1.53E-04	7.03E-03	6	HAND1, HEY1, ID4, LEF1, MSX1, MSX2
GO_POSITIVE_REGULATION_OF_MORPHOGENESIS_OF_AN_EPI_THELUM	1.56E-04	7.17E-03	5	GATA3, HOXB7, NOG, SOX9, WNT4
GO_REGULATION_OF_FAT_CELL_DIFFERENTIATION	1.57E-04	7.19E-03	9	GATA2, GATA3, GPER1, ID4, MSX2, PPARG, SNAI2, WNT3A, WNT5B
GO_CARDIAC_SEPTUM_MORPHOGENESIS	1.62E-04	7.34E-03	7	HAND1, HEY1, ISL1, LRP2, MSX2, NOG, TBX3
GO_MALE_SEX_DIFFERENTIATION	1.64E-04	7.41E-03	10	ADGRG1, GATA3, GREB1L, INHBA, LRP2, SOX9, TBX3, TCF21, WNT4, WNT9B
GO_NEGATIVE_REGULATION_OF_NEURON_DIFFERENTIATION	1.67E-04	7.49E-03	12	CNTN4, DIO3, DLX1, DLX2, EFN1, ID4, ISL1, MEIS1, SEMA6D, SLC6A4, SOX9, WNT3A
GO_CARDIAC_CHAMBER_MORPHOGENESIS	1.67E-04	7.49E-03	9	COL11A1, GATA3, HAND1, HEY1, ISL1, LRP2, MSX2, NOG, TBX3
GO_FOREBRAIN_NEURON_DIFFERENTIATION	1.69E-04	7.53E-03	6	CSF1R, DLX1, DLX2, DLX5, GATA2, INHBA
GO_VENTRICULAR_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	1.69E-04	7.53E-03	6	COL11A1, HAND1, ISL1, LRP2, NOG, TBX3
GO_CELL_MIGRATION_INVOLVED_IN_HEART_DEVELOPMENT	1.73E-04	7.63E-03	4	FLRT3, FOLR1, SNAI2, TWIST1
GO_DEFINITIVE_HEMOPOIESIS	1.73E-04	7.63E-03	4	GATA2, HOXB3, HOXB4, MEIS1
GO_NEURAL_TUBE_DEVELOPMENT	1.82E-04	7.96E-03	10	ALDH1A2, DLX1, FOLR1, GRHL3, LRP2, NOG, PLXNA2, TWIST1, WNT3A, ZEB2
GO_SEGMENTATION	1.84E-04	8.03E-03	8	ALDH1A2, CDX2, LEF1, OSR1, PLXNA2, TBX3, WNT3A, ZEB2
GO_MESENCHYMAL_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	1.87E-04	8.14E-03	3	OSR1, TCF21, WNT4
GO_PANCREAS_DEVELOPMENT	1.90E-04	8.23E-03	7	ALDH1A2, ANXA1, ISL1, MEIS2, PDX1, SOX9, WLS
GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT	2.01E-04	8.66E-03	10	COL11A1, COL19A1, COL3A1, COL6A6, HAPLN1, IGFBP7, LAMB3, LUM, POSTN, TNC
GO_OUTFLOW_TRACT_MORPHOGENESIS	2.06E-04	8.84E-03	7	FOLR1, ISL1, LRP2, MSX2, NOG, TBX3, TWIST1
GO_HEART_VALVE_DEVELOPMENT	2.08E-04	8.87E-03	6	EFNA1, GATA3, HEY1, SNAI2, SOX9, TWIST1
GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_REGULATORY_REGION_DNA_BINDING	2.14E-04	9.06E-03	4	HAND1, HEY1, MSX1, MSX2
GO_RENAL_VESICLE_DEVELOPMENT	2.14E-04	9.06E-03	4	OSR1, SOX9, WNT4, WNT9B
GO_POSITIVE_REGULATION_OF_SECRETION	2.25E-04	9.49E-03	17	ANKRD1, CD274, CSF1R, GATA2, GATA3, GPER1, INHBA, ISL1, LPL, NPPB, P2RY2, PDX1, POSTN, SLC6A4, TWIST1, VTCN1, WLS
GO_RESPONSE_TO_ACID_CHEMICAL	2.29E-04	9.62E-03	15	ALDH1A2, COL3A1, FOLR1, IGFBP7, OSR1, P2RY6, PDX1, PPARG, SLC6A4, SOX9, TNC, WNT3A, WNT5B, WNT6, WNT9B
GO_POSITIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	2.32E-04	9.69E-03	12	ANXA1, BMPER, CYP1B1, FGFBP1, GATA2, GPER1, ISL1, MYOCD, PRKD1, RUNX1, SPHK1, TWIST1
GO_CARDIOCYTE_DIFFERENTIATION	2.45E-04	1.02E-02	10	ACTC1, FOLR1, GPER1, ISL1, MYLK3, MYOCD, SLC8A1, TBX3, TWIST1, WNT3A
GO_CARDIAC_SEPTUM_DEVELOPMENT	2.72E-04	1.13E-02	8	GATA3, HAND1, HEY1, ISL1, LRP2, MSX2, NOG, TBX3
GO_EPIDERMIS_DEVELOPMENT	2.74E-04	1.13E-02	18	ANXA1, BNC1, GRHL3, HOXC13, INHBA, KRT16, KRT17, KRT23, KRT80, LAMB3, MSX2, RUNX1, SOX9, STS, TGM1, TNFRSF19, TP63, ZNF750
GO_REGULATION_OF_PEPTIDYL_LYSINE_ACETYLTATION	2.77E-04	1.14E-02	6	GATA2, GATA3, ISL1, MYOCD, SNAI2, TWIST1
GO_MESONEPHRIC_DUCT_DEVELOPMENT	2.78E-04	1.14E-02	3	GREB1L, OSR1, WNT9B
GO_ENDOPLASMIC_RETICULUM_LUMEN	2.89E-04	1.18E-02	14	CASQ2, COL11A1, COL19A1, COL3A1, ERP27, IGFBP3, IGFBP7, PRSS23, STS, TNC, WNT3A, WNT4, WNT5B, WNT6
GO_FRIZZLED_BINDING	3.04E-04	1.23E-02	5	WNT3A, WNT4, WNT5B, WNT6, WNT9B
GO_NEGATIVE_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	3.04E-04	1.23E-02	5	DLX1, DLX2, GATA2, HEY1, TCIM
GO_REGULATION_OF_HEART_MORPHOGENESIS	3.04E-04	1.23E-02	5	ISL1, NOG, SOX9, TWIST1, WNT3A
GO_CIRCULATORY_SYSTEM_PROCESS	3.15E-04	1.26E-02	20	ACTC1, ADRA1B, CACNG4, CASQ2, ENPEP, EPAS1, GPER1, GUCY1A1, HOXB2, MYLK3, MYOF, NPPB, NR2F2, P2RY2, POPDC2, POSTN, PPARG, SGC6, SLC6A4, SLC8A1
GO_POSITIVE_REGULATION_OF_MESONEPHROS_DEVELOPMENT	3.15E-04	1.26E-02	4	GATA3, HOXB7, NOG, SOX9
GO_UTERUS_DEVELOPMENT	3.15E-04	1.26E-02	4	GATA3, GREB1L, MYOCD, WNT9B
GO_SKELETAL_MUSCLE_ORGAN_DEVELOPMENT	3.26E-04	1.29E-02	10	ANKRD1, COL19A1, DMRTA2, MYOCD, NR2F2, PITX1, POPDC2, TCF21, TWIST1, WNT3A
GO_MOLTING_CYCLE	3.27E-04	1.29E-02	8	HOXC13, INHBA, KRT16, KRT17, MSX2, SOX9, TNFRSF19, TP63
GO_EMBRYONIC_DIGIT_MORPHOGENESIS	3.33E-04	1.31E-02	6	MSX1, MSX2, NOG, OSR1, TBX3, TWIST1
GO_POSITIVE_REGULATION_OF_EMBRYONIC_DEVELOPMENT	3.43E-04	1.34E-02	5	AMOT, GATA3, OSR1, WNT3A, WNT4
GO_NEGATIVE_REGULATION_OF_CELL_MOTILITY	3.64E-04	1.42E-02	15	ADGRG1, ARHGDIB, COL3A1, CYP1B1, DLX1, GATA3, IGFBP3, KRT16, MYOCD, NOG, NR2F2, PPARG, SEMA6D, TACSTD2, WNT4
GO_NEURAL_RETINA_DEVELOPMENT	3.64E-04	1.42E-02	6	DIO3, DLX1, DLX2, SOX9, TFAP2A, TFAP2B
GO_ENDOCARDIAL_CUSHION_FORMATION	3.77E-04	1.46E-02	4	MSX1, MSX2, NOG, SNAI2
GO_POSITIVE_REGULATION_OF_KIDNEY_DEVELOPMENT	3.86E-04	1.49E-02	5	GATA3, HOXB7, NOG, SOX9, WNT4
GO_TRANSCRIPTION_FACTOR_BINDING	3.88E-04	1.49E-02	22	ANKRD1, EPAS1, EYA2, GATA2, GATA3, HAND1, HEY1, HOXB4, ID4, ISL1, LEF1, MEIS2, MSX2, MYOCD, PDX1, PITX1, PPARG, SOX9, TBX3, TCF21, TWIST1, ZNF703
GO_FOREBRAIN_NEURON_FATE_COMMITMENT	3.92E-04	1.50E-02	3	DLX1, DLX2, GATA2
GO_NAIL_DEVELOPMENT	3.92E-04	1.50E-02	3	HOXC13, MSX1, MSX2
GO_EMBRYONIC_PLACENTA_DEVELOPMENT	4.02E-04	1.53E-02	7	CDX2, EPAS1, GATA2, HAND1, HEY1, LEF1, NR2F2
GO_MOLTING_CYCLE_PROCESS	4.30E-04	1.63E-02	7	HOXC13, INHBA, KRT17, MSX2, SOX9, TNFRSF19, TP63
GO_BONE_DEVELOPMENT	4.39E-04	1.66E-02	11	CSGALNACT1, DLX5, HOXB4, MEIS1, MSX1, MSX2, SOX9, SP5, TFAP2A, TWIST1, VIT
GO_G_PROTEIN_COUPLED_PURINERGIC_RECEPTOR_SIGNALING_PATHWAY	4.47E-04	1.68E-02	4	ACPP, GPR87, P2RY2, P2RY6
GO_REPRODUCTION	4.55E-04	1.70E-02	39	ADAM28, ADCY10, ADGRG1, ANXA1, ARHGDIB, BNC1, CDX2, CLIC5, DLX3, EPAS1, GATA2, GATA3, GREB1L, HAND1, HEY1, ID4, IGFBP7, INHBA, LEF1, LRP2, MSX1, MSX2, MYOCD, NOG, NR2F2, OSR1, PAPP, PLB1, PPARG, PRLR, SLC6A4, SOX9, STS, TBX3, TCF21, TNC, TP63, WNT4, WNT9B
GO_NEGATIVE_REGULATION_OF_LOCOMOTION	4.56E-04	1.70E-02	16	ADGRG1, ARHGDIB, COL3A1, CYP1B1, DLX1, GATA3, IGFBP3, KRT16, MYOCD, NOG, NR2F2, PPARG, SEMA6D, TACSTD2, WNT3A, WNT4
GO_TUBE_CLOSURE	4.61E-04	1.71E-02	7	DLX1, FOLR1, GRHL3, LRP2, NOG, TWIST1, ZEB2
GO_NEURAL_PRECURSOR_CELL_PROLIFERATION	4.64E-04	1.72E-02	9	ADGRG1, DMRTA2, GATA2, ID4, LEF1, LRP2, SLC6A4, WNT3A, ZEB2
GO_ANIMAL_ORGAN_FORMATION	4.71E-04	1.74E-02	6	FOLR1, ISL1, LRP2, NOG, TP63, WNT3A
GO_EXTRACELLULAR_MATRIX	4.80E-04	1.76E-02	19	ANXA1, COL11A1, COL19A1, COL3A1, COL6A6, COLEC12, FLRT3, HAPLN1, IGFBP7, LAMB3, LUM, POSTN, SERPINB8, TGM2, TNC, VIT, WNT4, WNT5B, WNT6
GO_STRIATED_MUSCLE_CELL_DIFFERENTIATION	4.87E-04	1.78E-02	13	ACTC1, ANKRD1, BAX2, CASQ2, LM2D, MSX1, MYLK3, MYOCD, MYOF, POPDC2, SLC8A1, TBX3, WNT3A
GO_CHONDROCYTE_DIFFERENTIATION	4.92E-04	1.79E-02	8	COL11A1, GDF6, MSX2, OSR1, SNAI2, SOX9, VIT, WNT5B
GO_PLACENTA_DEVELOPMENT	5.12E-04	1.86E-02	9	CDX2, DLX3, EPAS1, GATA2, HAND1, HEY1, LEF1, NR2F2, PPARG

GO_POSITIVE_REGULATION_OF_SIGNALING	5.14E-04	1.86E-02	46	ACKR3, ACPP, ADGRG1, ADRA1B, AFAP1L2, ANKRD1, BMPER, CACNG4, CCR1, CDKN2B, CLSTN2, COL3A1, CSF1R, CYP1B1, DKK2, DLX5, EFNA1, FGFBP1, GATA3, GDF6, GPER1, GUCY1A1, IGFBP3, IL18, IL1R1, INHBA, ISL1, JPH2, MAL, MSX1, MSX2, MYOCD, P2RY6, PDX1, PRKD1, PRLR, SOX9, SPHK1, TCIM, TGM2, TNFRSF19, TNFSF15, TP63, WLS, WNT3A, ZEB2
GO_FIBRILLAR_COLLAGEN_TRIMER	5.33E-04	1.92E-02	3	COL11A1, COL3A1, LUM
GO_METANEPHRIC_TUBULE_MORPHOGENESIS	5.33E-04	1.92E-02	3	SOX9, WNT4, WNT9B
GO_CELLULAR_RESPONSE_TO_OXYGEN_CONTAINING_COMPOUND	5.52E-04	1.97E-02	32	ALDH1A2, ANKRD1, ANXA1, CD274, COL3A1, COLEC12, CYP1B1, FOLR1, GPER1, IL18, INHBA, LPL, LTPD1, MSX2, OSR1, P2RY2, P2RY6, PDX1, PPARG, PRKD1, PRLR, SLC6A4, SLC8A1, SNAI2, SOX9, SPHK1, TNC, WNT3A, WNT5B, WNT6, WNT9B, ZNF703
GO_CRANIAL_SKELETAL_SYSTEM_DEVELOPMENT	5.55E-04	1.97E-02	6	DLX2, MSX2, TFAP2A, TP63, TWIST1, WNT9B
GO_RESPONSE_TO_NUTRIENT	5.55E-04	1.97E-02	11	ALDH1A2, CDKN2B, FOLR1, P2RY2, PDX1, POSTN, PPARG, SLC6A4, SLC8A1, SNAI2, TNC
GO_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_IN_CELL_CELL_SIGNALING	5.61E-04	1.98E-02	21	AMER2, DKK2, DLX5, FOLR1, GATA3, GRHL3, ISL1, LEFT1, NOG, RUNX1, SNAI2, SOX7, SOX9, WLS, WNT3A, WNT4, WNT5B, WNT6, WNT9B, ZEB2, ZNF703
GO_RESPONSE_TO_VITAMIN	5.62E-04	1.98E-02	7	ALDH1A2, FOLR1, PDX1, POSTN, PPARG, SNAI2, TNC
GO_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	5.81E-04	2.04E-02	8	ID4, MSX2, NOG, PRKD1, SNAI2, TP63, TWIST1, WNT4
GO_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA	5.87E-04	2.06E-02	12	ANKRD1, CDKN2B, COL3A1, DLX1, FOLR1, HTRA3, MYOCD, POSTN, SMAD9, SOX9, WNT4, ZNF703
GO_REGULATION_OF_BINDING	5.94E-04	2.08E-02	15	GATA3, GREM2, HAND1, HEY1, ID4, ISL1, LEFT1, MSX1, MSX2, MYOCD, NOG, PDX1, PPARG, TWIST1, WNT3A
GO_NEURON_FATE_COMMITMENT	6.01E-04	2.09E-02	6	DLX1, DLX2, DMRTA2, EVX1, GATA2, ISL1
GO_CELL_DIFFERENTIATION_INVOLVED_IN_METANEPHROS_DEVELOPMENT	6.14E-04	2.12E-02	4	OSR1, TCF21, WNT4, WNT9B
GO_NEGATIVE_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	6.14E-04	2.12E-02	4	DLX1, DLX2, ID4, NOG
GO_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	6.19E-04	2.13E-02	9	GATA3, MSX2, OSR1, RUNX1, SOX9, TBX3, TP63, WNT9B, ZEB2
GO_AUTONOMIC_NERVOUS_SYSTEM_DEVELOPMENT	6.63E-04	2.26E-02	5	GATA3, HOXB2, TFAP2A, TFAP2B, TP63
GO_GENITALIA_DEVELOPMENT	6.63E-04	2.26E-02	5	GREB1L, LRP2, TBX3, TP63, WNT9B
GO_POSITIVE_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	6.63E-04	2.26E-02	5	OSR1, SLC8A1, TFAP2A, WNT4, WNT6
GO_SKIN_DEVELOPMENT	6.79E-04	2.30E-02	16	ANXA1, COL3A1, GRHL3, HOXC13, INHBA, KRT16, KRT17, KRT23, KRT80, MSX2, RUNX1, SOX9, TFAP2B, TGM1, TNFRSF19, TP63
GO_ARTERY_DEVELOPMENT	6.80E-04	2.30E-02	7	COL3A1, FOLR1, HEY1, LRP2, MYOCD, NOG, TFAP2B
GO_POSITIVE_REGULATION_OF_CELL_DEATH	6.86E-04	2.32E-02	23	ADCY10, ALDH1A2, ANKRD1, ANXA1, CD274, CYP1B1, DLX1, GPER1, IGFBP3, INHBA, MAL, MSX1, MSX2, PDX1, PPARG, SOX7, TFAP2A, TFAP2B, TGM2, TNFSF15, TP63, UNC5C, WNT3A
GO_NEGATIVE_REGULATION_OF_OLIGODENDROCYTE_DIFFERENTIATION	7.03E-04	2.36E-02	3	DLX1, DLX2, ID4
GO_NEPHRIC_DUCT_MORPHOGENESIS	7.03E-04	2.36E-02	3	GATA3, OSR1, WNT9B
GO_BIOMINERAL_TISSUE_DEVELOPMENT	7.12E-04	2.37E-02	9	CCR1, MSX2, OSR1, SLC8A1, SOX9, TFAP2A, TWIST1, WNT4, WNT6
GO_METANEPHRIC_EPITHELIUM_DEVELOPMENT	7.12E-04	2.37E-02	4	OSR1, SOX9, WNT4, WNT9B
GO_REGULATION_OF_ODONTOGENESIS	7.12E-04	2.37E-02	4	MSX1, SP6, TFAP2A, WNT6
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	7.33E-04	2.43E-02	5	MSX2, OSR1, SOX9, TBX3, TP63
GO_CYTOKINE_BINDING	7.57E-04	2.50E-02	8	ACKR3, CCR1, CSF1R, CSF2RA, GREM2, IL1R1, NOG, PRLR
GO_RESPONSE_TO ESTRADIOL	7.97E-04	2.62E-02	8	ALDH1A2, ANXA1, GPER1, MSX2, NR2F2, POSTN, SLC6A4, ZNF703
GO_EXOCRINE_SYSTEM_DEVELOPMENT	8.08E-04	2.65E-02	5	PDX1, SNAI2, SOX9, TGM2, WLS
GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION	8.11E-04	2.65E-02	16	COL11A1, COL19A1, COL3A1, CSGALNACT1, CYP1B1, HAPLN1, ITGB6, LAMB3, LCP1, LPL, LUM, POSTN, SOX9, TNC, VIT, WNT3A
GO_SOMATIC_STEM_CELL_POPULATION_MAINTENANCE	8.15E-04	2.65E-02	6	CDX2, GATA2, NOG, SOX9, TP63, WNT9B
GO_REGULATION_OF_PROTEIN_ACETYLATION	8.77E-04	2.84E-02	6	GATA2, GATA3, ISL1, MYOCD, SNAI2, TWIST1
GO_SOMITOGENESIS	8.77E-04	2.84E-02	6	ALDH1A2, CDX2, LEFT1, PLXNA2, WNT3A, ZEB2
GO_EXTRACELLULAR_MATRIX_COMPONENT	8.89E-04	2.87E-02	5	COL11A1, COL3A1, LAMB3, LUM, TNC
GO_CELLULAR_RESPONSE_TO_PURINE_CONTAINING_COMPOUND	9.04E-04	2.88E-02	3	CASQ2, P2RY6, SLC8A1
GO_CO_RECEPTOR_BINDING	9.04E-04	2.88E-02	3	DKK2, WNT3A, WNT9B
GO_MESENCHYMAL_CELL_APOPTOTIC_PROCESS	9.04E-04	2.88E-02	3	MSX1, MSX2, SOX9
GO_POSITIVE_REGULATION_OF_MEIOTIC_NUCLEAR_DIVISION	9.04E-04	2.88E-02	3	MSX1, MSX2, WNT4
GO_SEX_DIFFERENTIATION	9.07E-04	2.88E-02	12	ADGRG1, GATA3, GREB1L, INHBA, LRP2, OSR1, SOX9, TBX3, TCF21, TP63, WNT4, WNT9B
GO_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	9.20E-04	2.91E-02	7	DLX1, DLX2, GATA2, HEY1, POSTN, TCIM, TP63
GO_CARTILAGE_MORPHOGENESIS	9.41E-04	2.97E-02	4	HAND1, MSX1, SNAI2, VIT
GO_REGULATION_OF_EMBRYONIC_DEVELOPMENT	9.74E-04	3.05E-02	8	AMOT, CDX2, GATA2, GATA3, GRHL3, OSR1, WNT3A, WNT4
GO_ENDODERM_FORMATION	9.75E-04	3.05E-02	5	COL11A1, INHBA, LAMB3, NOG, SOX7
GO_E_BOX_BINDING	9.75E-04	3.05E-02	5	GATA3, PPARG, SNAI2, TCF21, TWIST1
GO_NEURON_PROJECTION_GUIDANCE	9.99E-04	3.11E-02	12	CNTN4, CSF1R, DLX5, EFNA1, FLRT3, GATA3, ISL1, NOG, PLXNA2, SEMA6D, UNC5C, WNT3A
GO_POSITIVE_REGULATION_OF_PEPTIDE_SECRETION	1.06E-03	3.30E-02	12	ANKRD1, CD274, CSF1R, GATA3, GPER1, ISL1, LPL, PDX1, POSTN, TWIST1, VTCN1, WLS
GO_BODY_MORPHOGENESIS	1.07E-03	3.30E-02	5	DLX5, GREM2, LEFT1, MSX1, NOG
GO_HEART_FORMATION	1.07E-03	3.30E-02	4	FOLR1, ISL1, LRP2, WNT3A
GO_REGULATION_OF_KERATINOCYTE_PROLIFERATION	1.07E-03	3.30E-02	4	PRKD1, SNAI2, TGM1, TP63
GO_POSITIVE_REGULATION_OF_REPRODUCTIVE_PROCESS	1.08E-03	3.32E-02	6	INHBA, MSX1, MSX2, PLB1, SOX9, WNT4
GO_NEURAL_TUBE_FORMATION	1.09E-03	3.33E-02	7	DLX1, FOLR1, GRHL3, LRP2, NOG, TWIST1, ZEB2
GO_SPINAL_CORD_DEVELOPMENT	1.09E-03	3.33E-02	7	EVX1, GATA2, HOXB8, ISL1, NOG, VIT, WNT3A
GO_CARDIAC_CELL_FATE_COMMITMENT	1.14E-03	3.42E-02	3	ISL1, TBX3, WNT3A
GO_G_PROTEIN_COUPLED_NUCLEOTIDE_RECEPTOR_ACTIVITY	1.14E-03	3.42E-02	3	GPR87, P2RY2, P2RY6
GO_G_PROTEIN_COUPLED_PURINERGIC_NUCLEOTIDE_RECEPTOR_SIGNALING_PATHWAY	1.14E-03	3.42E-02	3	GPR87, P2RY2, P2RY6
GO_T_HELPER_2_CELL_DIFFERENTIATION	1.14E-03	3.42E-02	3	ANXA1, GATA3, IL18
GO_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	1.16E-03	3.48E-02	6	GPER1, HEY1, MYOCD, PRDM6, SOX9, WNT4
GO_REGULATION_OF_MYOBlast_DIFFERENTIATION	1.27E-03	3.81E-02	5	IGFBP3, IL18, MYOCD, SOX9, TBX3
GO_PALLIUM_DEVELOPMENT	1.35E-03	4.04E-02	9	ADGRG1, COL3A1, DLX1, DLX2, DMRTA2, ID4, LEFT1, WNT3A, ZEB2
GO_FACE_MORPHOGENESIS	1.37E-03	4.04E-02	4	DLX5, LEFT1, MSX1, NOG
GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTILE_FUNCTION	1.37E-03	4.04E-02	4	ADRA1B, GPER1, MYOCD, SPHK1
GO_PURINERGIC_RECEPTOR_SIGNALING_PATHWAY	1.37E-03	4.04E-02	4	ACPP, GPR87, P2RY2, P2RY6
GO_REGULATION_OF_DNA_DAMAGE_RESPONSE_SIGNAL_TRANSDUCTION_BY_P53_CLASS_MEDIATOR	1.37E-03	4.04E-02	4	ANKRD1, MSX1, SNAI2, TWIST1
GO_REGULATION_OF_OLIGODENDROCYTE_DIFFERENTIATION	1.37E-03	4.04E-02	4	DLX1, DLX2, ID4, PPARG
GO_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	1.39E-03	4.06E-02	5	GATA3, OSR1, TCF21, WNT4, WNT9B
GO_ORGANIC_HYDROXY_COMPOUND_METABOLIC_PROCESS	1.39E-03	4.07E-02	17	ACADL, ALDH1A2, ALDH3B2, CYP1B1, DIO2, DIO3, EPAS1, GATA3, GPER1, LRP2, MYOF, P2RY6, PLB1, SNAI2, SPHK1, WNT4, ZEB2
GO_HEART_FIELD_SPECIFICATION	1.41E-03	4.07E-02	3	ISL1, LRP2, WNT3A
GO_METANEPHRIC_MESENCHYME_DEVELOPMENT	1.41E-03	4.07E-02	3	OSR1, TCF21, WNT4
GO_POSITIVE_REGULATION_OF_CHEMOKINE_SECRETION	1.41E-03	4.07E-02	3	CSF1R, LPL, POSTN
GO_LIMBIC_SYSTEM_DEVELOPMENT	1.44E-03	4.15E-02	7	DLX1, DLX2, ID4, LEFT1, TBX3, WNT3A, ZEB2
GO_GLIOGENESIS	1.45E-03	4.16E-02	12	ADGRG1, ANXA1, CSF1R, DLX1, DLX2, ID4, LEFT1, LRP2, NOG, PPARG, SH3TC2, SOX9
GO_REGULATION_OF_TUBE_SIZE	1.49E-03	4.28E-02	8	ADRA1B, GPER1, GUCY1A1, NPPB, P2RY2, SLC6A4, SLC8A1, WNT9B
GO_HIPPOCAMPUS_DEVELOPMENT	1.51E-03	4.32E-02	6	DLX1, DLX2, ID4, LEFT1, WNT3A, ZEB2

GO INTERFERON GAMMA PRODUCTION	1.51E-03	4.33E-02	7	CD274, GATA3, IL18, IL1R1, INHBA, ISL1, VTCN1
GO MAMMARY GLAND DUCT MORPHOGENESIS	1.55E-03	4.40E-02	4	CSF1R, MSX2, TBX3, WNT4
GO COLLAGEN CONTAINING EXTRACELLULAR MATRIX	1.55E-03	4.40E-02	15	ANXA1, COL11A1, COL19A1, COL3A1, COL6A6, HAPLN1, IGFBP7, LAMB3, LUM, POSTN, SERPINB8, TGM2, TNC, VIT, WNT5B
GO POSITIVE REGULATION OF CYTOKINE PRODUCTION	1.58E-03	4.48E-02	16	AFAP1L2, ANXA1, CD274, CSF1R, CYP1B1, GATA3, IL18, IL1R1, ISL1, LPL, LUM, POSTN, RUNX1, TWIST1, VTCN1, WNT34
GO BONE MINERALIZATION	1.60E-03	4.51E-02	7	CCRI, OSR1, SLC8A1, SOX9, TFAP2A, TWIST1, WNT4
GO REGULATION OF MORPHOGENESIS OF A BRANCHING STRUCTURE	1.63E-03	4.60E-02	5	HOXB7, NOG, SNAI2, SOX9, TACSTD2
GO REGULATION OF STEM CELL DIFFERENTIATION	1.68E-03	4.72E-02	7	GATA2, GATA3, HOXB4, RUNX1, SOX9, TACSTD2, WNT34
GO DIGESTIVE SYSTEM DEVELOPMENT	1.70E-03	4.77E-02	8	ALDH1A2, CDX2, COL3A1, MYOCD, PDX1, TCF21, TP63, WLS
GO THYROID HORMONE GENERATION	1.71E-03	4.78E-02	3	DIO2, DIO3, GATA3
GO NEGATIVE REGULATION OF ANIMAL ORGAN MORPHOGENESIS	1.73E-03	4.81E-02	4	DIO3, GATA3, NOG, TACSTD2
GO SPLEEN DEVELOPMENT	1.73E-03	4.81E-02	4	CDKN2B, HOXB4, SLC40A1, TCF21
GO NEURAL CREST CELL MIGRATION	1.77E-03	4.89E-02	5	FOLR1, ISL1, SEMA6D, TWIST1, ZEB2
GO REGULATION OF MORPHOGENESIS OF AN EPITHELIUM	1.78E-03	4.93E-02	9	GATA3, GRHL3, HOXB7, NOG, SNAI2, SOX9, TACSTD2, WNT4, WNT9B
GO CELL FATE SPECIFICATION	1.82E-03	5.01E-02	6	DMRTA2, EYX1, EY42, ISL1, SOX9, WNT3A
GO REGULATION OF CD4 POSITIVE ALPHA BETA T CELL ACTIVATION	1.91E-03	5.25E-02	5	ANXA1, CD274, GATA3, IL18, RUNX1
GO DENDRITIC SHAFT	1.93E-03	5.28E-02	4	GPRI1, MAP1A, SLC8A1, ZNF804A
GO CHEMOKINE PRODUCTION	1.93E-03	5.28E-02	6	CSF1R, IL18, LPL, POSTN, SNAI2, TWIST1
GO TAXIS	1.95E-03	5.31E-02	20	ACKR3, AMOT, ANXA1, CCRI, CNTN4, CSF1R, DLX5, EFN1, FLRT3, GATA3, HOXB9, ISL1, LEF1, NOG, PIK3C2G, PLXNA2, PRKD1, SEMA6D, UNC5C, WNT3A
GO RESPONSE TO DRUG	1.99E-03	5.39E-02	28	ABCG2, ACTC1, ANKRD1, ANXA1, CA3, CACNG4, CASQ2, CYP1B1, FOLR1, GATA3, IGFBP7, INHBA, LPL, LRP2, LYPD1, MSX1, NNMT, OSR1, P2RY2, PDX1, PPARG, RAB6C, SLC6A4, SLC8A1, SOX9, SPHK1, TFAP2B, TNC
GO CELLULAR RESPONSE TO EXTERNAL STIMULUS	2.05E-03	5.50E-02	13	ANKRD1, CDKN2B, FOLR1, MYOCD, P2RY2, POSTN, PPARG, PRKD1, SNAI2, SOX9, TNC, WNT4, WNT9B
GO REGULATION OF NEURAL PRECURSOR CELL PROLIFERATION	2.05E-03	5.50E-02	6	ADGRG1, DMRTA2, GATA2, LRP2, SLC6A4, WNT3A
GO FEMALE GENITALIA DEVELOPMENT	2.05E-03	5.50E-02	3	LRP2, TBX3, TP63
GO NEGATIVE REGULATION OF KIDNEY DEVELOPMENT	2.05E-03	5.50E-02	3	GATA3, OSR1, TACSTD2
GO RESPONSE TO CAFFEINE	2.05E-03	5.50E-02	3	CASQ2, PPARG, SLC8A1
GO CD4 POSITIVE ALPHA BETA T CELL ACTIVATION	2.18E-03	5.80E-02	6	ANXA1, CD274, GATA3, IL18, LEF1, RUNX1
GO COLLAGEN TRIMER	2.18E-03	5.80E-02	6	COL11A1, COL19A1, COL3A1, COL6A6, COLEC12, LUM
GO 3 CHLOROALLYL ALDEHYDE DEHYDROGENASE ACTIVITY	2.26E-03	5.89E-02	2	ALDH1A2, ALDH3B2
GO DUCTUS ARTERIOSUS CLOSURE	2.26E-03	5.89E-02	2	MYOCD, TFAP2B
GO ESTROGEN RECEPTOR ACTIVITY	2.26E-03	5.89E-02	2	GPRI1, LEF1
GO FOLATE IMPORT ACROSS PLASMA MEMBRANE	2.26E-03	5.89E-02	2	FOLR1, LRP2
GO MYOBLAST FATE COMMITMENT	2.26E-03	5.89E-02	2	EPAS1, PITX1
GO NEPHRIC DUCT FORMATION	2.26E-03	5.89E-02	2	GATA3, WNT9B
GO POSITIVE REGULATION OF CARDIAC VASCULAR SMOOTH MUSCLE CELL DIFFERENTIATION	2.26E-03	5.89E-02	2	GPRI1, MYOCD
GO REGULATION OF T HELPER 1 CELL CYTOKINE PRODUCTION	2.26E-03	5.89E-02	2	IL18, IL1R1
GO STEM CELL PROLIFERATION	2.26E-03	5.89E-02	7	DMRTA2, ID4, LEF1, RUNX1, SNAI2, TBX3, WNT3A
GO DITERPENOID METABOLIC PROCESS	2.31E-03	5.99E-02	6	ABC44, ALDH1A2, CYP1B1, LPL, LRP2, PLB1
GO POSITIVE REGULATION OF BONE MINERALIZATION	2.38E-03	6.14E-02	4	OSR1, SLC8A1, TFAP2A, WNT4
GO REGULATION OF FIBROBLAST GROWTH FACTOR RECEPTOR SIGNALING PATHWAY	2.38E-03	6.14E-02	4	FGFBP1, GATA3, NOG, WNT4
GO NEGATIVE REGULATION OF MUSCLE TISSUE DEVELOPMENT	2.39E-03	6.16E-02	5	LEF1, MEIS1, MYOCD, NOG, TWIST1
GO POSITIVE REGULATION OF T CELL CYTOKINE PRODUCTION	2.44E-03	6.24E-02	3	GATA3, IL18, IL1R1
GO POST ANAL TAIL MORPHOGENESIS	2.44E-03	6.24E-02	3	SP5, TP63, WNT3A
GO REGULATION OF NEURON DIFFERENTIATION	2.51E-03	6.41E-02	20	ANKRD1, CNTN4, DIO3, DLX1, DLX2, EFN1, GATA2, GATA3, GDF6, ID4, ISL1, MEIS1, PLXNA2, PRKD1, SEMA6D, SLC6A4, SOX9, WNT3A, ZEB2, ZNF804A
GO NEGATIVE REGULATION OF RESPONSE TO STIMULUS	2.57E-03	6.53E-02	40	ACKR3, ADAMTS18, AMER2, ANXA1, BMPER, CASQ2, COL3A1, DKK2, DLX1, DLX2, EFN1, EY42, GATA2, GATA3, GPRI1, GPRC5A, GREM2, HEY1, HTRA3, IGFBP3, ISL1, LPL, LRP2, MYOCD, NOG, OSR1, PDX1, PPARG, RGS5, SEMA6D, SNAI2, SOX9, TCF21, TCIM, TP63, TWIST1, WNT3A, WNT4, WNT5B
GO POSITIVE REGULATION OF OSTEOBLAST DIFFERENTIATION	2.57E-03	6.53E-02	5	ID4, MSX2, PRKD1, TP63, WNT4
GO NEGATIVE REGULATION OF SIGNALING	2.61E-03	6.62E-02	35	ACKR3, AMER2, BMPER, CASQ2, DKK2, DLX1, DLX2, EFN1, EY42, GATA2, GATA3, GPRI1, GPRC5A, GREM2, HEY1, HTRA3, IGFBP3, INHBA, ISL1, LRP2, MYOCD, NOG, PDX1, PPARG, RGS5, SLC6A4, SNAI2, SOX9, TCF21, TCIM, TP63, TWIST1, WNT4, WNT5B
GO HEAD MORPHOGENESIS	2.63E-03	6.65E-02	4	DLX5, LEF1, MSX1, NOG
GO REGULATION OF EPITHELIAL TO MESENCHYMAL TRANSITION	2.73E-03	6.89E-02	6	EFNA1, ISL1, LEF1, NOG, TWIST1, ZNF703
GO CELLULAR RESPONSE TO EXTRACELLULAR STIMULUS	2.74E-03	6.89E-02	11	CDKN2B, FOLR1, MYOCD, P2RY2, POSTN, PPARG, PRKD1, SNAI2, TNC, WNT4, WNT9B
GO INTERLEUKIN 2 PRODUCTION	2.75E-03	6.92E-02	5	ANXA1, GATA3, IL18, RUNX1, VTCN1
GO TRANSCRIPTION COREGULATOR ACTIVITY	2.77E-03	6.93E-02	18	ANKRD1, CDX2, GATA3, HAND1, HEY1, HR, ID4, ISL1, MEIS2, MSX2, MYOCD, NR2F2, PPARG, TFAP2A, TFAP2B, VGLL1, WNT3A, WNT4
GO CARDIOBLAST DIFFERENTIATION	2.86E-03	7.06E-02	3	ISL1, MYOCD, WNT3A
GO CHEMOKINE SECRETION	2.86E-03	7.06E-02	3	CSF1R, LPL, POSTN
GO COMPLEX OF COLLAGEN TRIMERS	2.86E-03	7.06E-02	3	COL11A1, COL3A1, LUM
GO KIDNEY MESENCHYME DEVELOPMENT	2.86E-03	7.06E-02	3	OSR1, TCF21, WNT4
GO NOTOCHORD DEVELOPMENT	2.86E-03	7.06E-02	3	EFNA1, NOG, SOX9
GO REGULATION OF EPITHELIAL CELL DIFFERENTIATION INVOLVED IN KIDNEY DEVELOPMENT	2.86E-03	7.06E-02	3	GATA3, OSR1, WNT9B
GO RESPONSE TO OXYGEN CONTAINING COMPOUND	2.98E-03	7.35E-02	39	ACTC1, ALDH1A2, ANKRD1, ANXA1, CA3, CACNG4, CD274, COL3A1, COLEC12, CYP1B1, FOLR1, GATA3, GPRI1, IGFBP7, IL18, INHBA, LPL, LYPD1, MSX2, NR2F2, OSR1, P2RY2, P2RY6, PDX1, POSTN, PPARG, PRKD1, PRLR, SLC6A4, SLC8A1, SNAI2, SOX9, SPHK1, TNC, WNT3A, WNT5B, WNT6, WNT9B, ZNF703
GO ENDOTHELIAL CELL MIGRATION	3.07E-03	7.52E-02	11	AMOT, ANXA1, BMPER, CYP1B1, EFN1, FGFBP1, GATA2, GATA3, NR2F2, PPARG, PRKD1
GO NOTCH SIGNALING PATHWAY	3.07E-03	7.52E-02	9	DLX1, DLX2, GATA2, HEY1, POSTN, SNAI2, SOX9, TCIM, TP63
GO REGULATION OF SMOOTH MUSCLE CONTRACTION	3.16E-03	7.72E-02	5	ADRA1B, GPRI1, GUCY1A1, MYOCD, SPHK1
GO KERATINOCYTE PROLIFERATION	3.18E-03	7.73E-02	4	PRKD1, SNAI2, TGM1, TP63
GO REGENERATION	3.18E-03	7.73E-02	9	ANXA1, FOLR1, ISL1, LCPI, NNMT, PDX1, POSTN, PPARG, TNC
GO CYTOKINE PRODUCTION	3.21E-03	7.80E-02	22	ADGRG1, AFAP1L2, ANXA1, CD274, CSF1R, CYP1B1, GATA3, IL18, IL1R1, INHBA, ISL1, ITGB6, LEF1, LPL, LUM, POSTN, RUNX1, SNAI2, SPHK1, TWIST1, VTCN1, WNT3A
GO POSITIVE REGULATION OF TRANSPORT	3.28E-03	7.86E-02	26	ANKRD1, ANXA1, CACNG4, CCRI, CD274, CSF1R, GATA2, GATA3, GPRI1, INHBA, ISL1, JPH2, LPL, NPPB, P2RY2, P2RY6, PDX1, POSTN, PPARG, SLC6A4, TCA2, TP63, TWIST1, VTCN1, WLS, WNT3A
GO RESPIRATORY SYSTEM DEVELOPMENT	3.29E-03	7.86E-02	9	ALDH1A2, DLX5, EPAS1, LEF1, MYOCD, NOG, SOX9, TCF21, TNC
GO CARDIAC RIGHT VENTRICLE MORPHOGENESIS	3.33E-03	7.86E-02	3	GATA3, HAND1, ISL1
GO CD4 POSITIVE ALPHA BETA T CELL CYTOKINE PRODUCTION	3.33E-03	7.86E-02	3	GATA3, IL18, IL1R1

GO MESENCHYMAL TO EPITHELIAL TRANSITION	3.33E-03	7.86E-02	3	GATA3, WNT4, WNT9B
GO MIDDLE EAR MORPHOGENESIS	3.33E-03	7.86E-02	3	MSX1, NOG, OSR1
GO POSITIVE REGULATION OF STEM CELL DIFFERENTIATION	3.33E-03	7.86E-02	3	HOXB4, SOX9, TACSTD2
GO POSITIVE REGULATION OF T_HELPER_1_TYPE_IMMUNE_RESPONSE	3.33E-03	7.86E-02	3	ANXA1, IL18, IL1R1
GO THYROID HORMONE METABOLIC PROCESS	3.33E-03	7.86E-02	3	DIO2, DIO3, GATA3
GO FOLATE TRANSMEMBRANE TRANSPORT	3.36E-03	7.86E-02	2	FOLR1, LRP2
GO INTERLEUKIN 4 SECRETION	3.36E-03	7.86E-02	2	GATA3, VTCN1
GO ODONTOBLAST DIFFERENTIATION	3.36E-03	7.86E-02	2	DLX3, LEF1
GO PARAXIAL MESODERM FORMATION	3.36E-03	7.86E-02	2	LEF1, WNT3A
GO REGULATION OF CARDIAC_VASCULAR_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	3.36E-03	7.86E-02	2	GPRI1, MYOCD
GO URETERIC BUD FORMATION	3.36E-03	7.86E-02	2	GATA3, NOG
GO EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT_CONFERRING_TENSILE_STRENGTH	3.48E-03	8.10E-02	4	COL11A1, COL19A1, COL3A1, COL6A6
GO T_HELPER_1_TYPE_IMMUNE_RESPONSE	3.48E-03	8.10E-02	4	ANXA1, IL18, IL1R1, LEF1
GO POSITIVE REGULATION OF INTRACELLULAR SIGNAL TRANSDUCTION	3.57E-03	8.29E-02	27	ACKR3, ADGRG1, ADRA1B, ANKRD1, BMPER, CCR1, COL3A1, CSF1R, EFNA1, GATA3, GDF6, GPRI1, GUCY1A1, IGF1R, IL18, JPH2, MSX1, P2RY6, PRKD1, SOX9, SPHK1, TCIM, TGM2, TNFRSF19, TNFSF15, WLS, ZEB2
GO TRANSCRIPTION_FACTOR_COMPLEX	3.62E-03	8.39E-02	13	ANKRD1, BARX2, EPAS1, HAND1, HOXB9, LEF1, MEIS1, PITX1, PPARG, RUNX1, SMAD9, SOX7, SOX9
GO ACTIN FILAMENT	3.75E-03	8.69E-02	6	ACTC1, AMOT, ANXA1, LCPI, LMOD2, PSTPIP2
GO_RESPONSE_TO_WOUNDING	3.77E-03	8.70E-02	20	ADAMTS18, ANXA1, CCR1, COL3A1, CSRP1, FLRT3, FOLR1, GATA2, GATA3, GRHL3, ISL1, MSX2, MYOF, NOG, PDX1, POSTN, TNC, WNT3A, WNT4, WNT5B
GO NEGATIVE REGULATION OF BINDING	3.81E-03	8.74E-02	8	HAND1, HEY1, ID4, ISL1, LEF1, MSX1, MSX2, NOG
GO NEGATIVE REGULATION OF CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	3.81E-03	8.74E-02	8	BMPER, DLX1, GATA3, GREM2, HTRA3, LRP2, NOG, WNT4
GO CELL AGGREGATION	3.84E-03	8.74E-02	3	BARX2, COL11A1, SOX9
GO NUCLEOTIDE RECEPTOR ACTIVITY	3.84E-03	8.74E-02	3	GPRI1, P2RY2, P2RY6
GO SMOOTH MUSCLE TISSUE DEVELOPMENT	3.84E-03	8.74E-02	3	COL3A1, OSR1, SOX9
GO SYMPATHETIC NERVOUS SYSTEM DEVELOPMENT	3.84E-03	8.74E-02	3	GATA3, TFAP2B, TP63
GO POSITIVE REGULATION OF CYTOKINE SECRETION	4.06E-03	9.21E-02	7	CD274, CSF1R, GATA3, LPL, POSTN, TWIST1, VTCN1
GO NEGATIVE REGULATION OF GLOIENESIS	4.14E-03	9.38E-02	4	DLX1, DLX2, ID4, NOG
GO VASCULAR PROCESS IN CIRCULATORY SYSTEM	4.24E-03	9.60E-02	8	ADRA1B, GPRI1, GUCY1A1, MYLK3, NPPB, P2RY2, SLC6A4, SLC8A1
GO_CELL_CELL_ADHESION	4.32E-03	9.74E-02	23	ADAMTS18, ANXA1, CD274, CDH10, CLSTN2, CNTN4, COL19A1, CSRP1, CYP1B1, FLRT3, GATA3, IL18, LEF1, NECTIN4, RUNX1, SERPINB8, SNAI2, SOX9, TACSTD2, VTCN1, WNT3A, WNT4, ZNF703
GO MYELOID_CELL_DIFFERENTIATION	4.35E-03	9.74E-02	14	CCR1, CDKN2B, CSF1R, EPAS1, GATA2, GATA3, HOXB7, HOXB8, INHBA, LEF1, MEIS1, MEIS2, PPARG, RUNX1
GO MYOFIBRIL ASSEMBLY	4.35E-03	9.74E-02	5	ACTC1, ANKRD1, CASQ2, LMOD2, MYLK3
GO REGULATION OF GLIAL CELL DIFFERENTIATION	4.35E-03	9.74E-02	5	DLX1, DLX2, ID4, NOG, PPARG
GO CELLULAR RESPONSE TO PROSTAGLANDIN STIMULUS	4.40E-03	9.74E-02	3	P2RY6, PPARG, TNC
GO CYCLIC NUCLEOTIDE BIOSYNTHETIC PROCESS	4.40E-03	9.74E-02	3	ADCY10, GUCY1A1, NPPB
GO MALE GENITALIA DEVELOPMENT	4.40E-03	9.74E-02	3	GREB1L, TBX3, WNT9B
GO POSITIVE REGULATION OF MEIOTIC CELL CYCLE	4.40E-03	9.74E-02	3	MSX1, MSX2, WNT4
GO PURINERGIC_NUCLEOTIDE_RECEPTOR_SIGNALING_PATHWAY	4.40E-03	9.74E-02	3	GPRI1, P2RY2, P2RY6
GO GOLGI LUMEN	4.58E-03	1.00E-01	6	LUM, MUC15, WNT3A, WNT4, WNT5B, WNT6
GO_CARDIAC_NEURAL_CREAST_CELL_MIGRATION_INVOLVED_IN_OUTFLOW_TRACT_MORPHOGENESIS	4.65E-03	1.00E-01	2	FOLR1, TWIST1
GO CEREBRAL CORTEX REGIONALIZATION	4.65E-03	1.00E-01	2	ADGRG1, DMRTA2
GO EXOCRINE PANCREAS DEVELOPMENT	4.65E-03	1.00E-01	2	PDX1, WLS
GO FOLLICLE STIMULATING HORMONE SECRETION	4.65E-03	1.00E-01	2	INHBA, TBX3
GO JUNCTIONAL MEMBRANE COMPLEX	4.65E-03	1.00E-01	2	CASQ2, JPH2
GO NEGATIVE REGULATION OF MACROPHAGE DIFFERENTIATION	4.65E-03	1.00E-01	2	GATA2, INHBA
GO POSITIVE REGULATION OF TOOTH MINERALIZATION	4.65E-03	1.00E-01	2	TFAP2A, WNT6
GO REGULATION OF INOSITOL TRISPHOSPHATE BIOSYNTHETIC PROCESS	4.65E-03	1.00E-01	2	GPRI1, P2RY6
GO REGULATION OF RETINA DEVELOPMENT IN CAMERA TYPE EYE	4.65E-03	1.00E-01	2	DLX1, DLX2
GO RHOMBOMERE DEVELOPMENT	4.65E-03	1.00E-01	2	HOXB2, HOXB3
GO T_HELPER_1_CELL_CYTOKINE_PRODUCTION	4.65E-03	1.00E-01	2	IL18, IL1R1
GO URETER MORPHOGENESIS	4.65E-03	1.00E-01	2	GATA3, SOX9
GO_RESPONSE_TO_MECHANICAL_STIMULUS	4.70E-03	1.01E-01	9	ANKRD1, COL11A1, COL3A1, MEIS2, POSTN, PPARG, SLC8A1, SOX9, TNC
GO REGULATION OF EPITHELIAL_CELL_MIGRATION	4.85E-03	1.04E-01	11	ANXA1, BMPER, EFNA1, FGF1P1, GATA2, GATA3, NR2F2, PPARG, PRKD1, SOX9, TACSTD2
GO VENTRICULAR SEPTUM DEVELOPMENT	4.91E-03	1.05E-01	5	GATA3, HEY1, LRP2, NOG, TBX3
GO CEREBRAL CORTEX NEURON DIFFERENTIATION	5.00E-03	1.06E-01	3	DLX1, DLX2, ID4
GO R SMAD BINDING	5.00E-03	1.06E-01	3	ANKRD1, MYOCD, ZEB2
GO SEX DETERMINATION	5.00E-03	1.06E-01	3	SOX9, TCF21, WNT4
GO TOOTH MINERALIZATION	5.00E-03	1.06E-01	3	MSX2, TFAP2A, WNT6
GO MUSCLE_CELL_MIGRATION	5.04E-03	1.06E-01	6	ANXA1, IGF1P3, MYOCD, P2RY6, POSTN, SEMA6D
GO POSITIVE REGULATION OF TRANSMEMBRANE RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	5.04E-03	1.06E-01	6	CDKN2B, GDF6, INHBA, MSX1, MSX2, MYOCD
GO ISOPRENOL METABOLIC PROCESS	5.28E-03	1.11E-01	6	ABC44, ALDH1A2, CYP1B1, LPL, LRP2, PLB1
GO EMBRYONIC CRANIAL SKELETON MORPHOGENESIS	5.28E-03	1.11E-01	4	DLX2, TFAP2A, TWIST1, WNT9B
GO MAMMARY GLAND MORPHOGENESIS	5.28E-03	1.11E-01	4	CSF1R, MSX2, TBX3, WNT4
GO AXON DEVELOPMENT	5.29E-03	1.11E-01	16	CNTN4, CSF1R, DLX5, EFNA1, FLRT3, FOLR1, GATA3, ISL1, MAP1A, NOG, PLXNA2, SEMA6D, TNC, UNC5C, WNT3A, ZEB2
GO ENDODERM DEVELOPMENT	5.51E-03	1.15E-01	5	COL11A1, INHBA, LAMB3, NOG, SOX7
GO POSITIVE REGULATION OF SMALL MOLECULE METABOLIC PROCESS	5.53E-03	1.15E-01	6	ANXA1, GPRI1, P2RY6, PPARG, TWIST1, WNT4
GO_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	5.56E-03	1.16E-01	13	ACKR3, AMOT, ANXA1, CCR1, CD274, CSF2R4, ENPEP, FOLR1, IL1R1, ITGB6, LRP2, PRLR, VTCN1
GO ATRIOVENTRICULAR VALVE DEVELOPMENT	5.65E-03	1.17E-01	3	EFNA1, HEY1, TWIST1
GO INTERLEUKIN 13 PRODUCTION	5.65E-03	1.17E-01	3	GATA3, IL18, LEF1
GO REGULATION OF WATER LOSS VIA SKIN	5.65E-03	1.17E-01	3	GRHL3, KRT16, TP63
GO SOMATIC STEM CELL DIVISION	5.65E-03	1.17E-01	3	HOXB4, LEF1, WNT3A
GO CHONDROCYTE DEVELOPMENT	5.70E-03	1.17E-01	4	COL11A1, MSX2, SOX9, VIT
GO REGULATION OF CD4 POSITIVE ALPHA BETA T CELL DIFFERENTIATION	5.70E-03	1.17E-01	4	ANXA1, GATA3, IL18, RUNX1
GO REGULATION OF HISTONE MODIFICATION	5.82E-03	1.19E-01	7	GATA2, GATA3, ISL1, MYOCD, PRKD1, SNAI2, TWIST1
GO DNA BINDING TRANSCRIPTION_FACTOR_BINDING	6.07E-03	1.23E-01	12	ANKRD1, HAND1, HOXB4, ISL1, LEF1, MYOCD, PPARG, SOX9, TBX3, TCF21, TWIST1, ZNF703
GO AMACRINE CELL DIFFERENTIATION	6.14E-03	1.23E-01	2	DLX1, DLX2
GO FOLIC ACID TRANSPORT	6.14E-03	1.23E-01	2	FOLR1, LRP2
GO FOREBRAIN NEUROBLAST DIVISION	6.14E-03	1.23E-01	2	LEF1, WNT3A
GO METANEPHRIC_GLOMERULUS_VASCULATURE_DEVELOPMENT	6.14E-03	1.23E-01	2	OSR1, TCF21
GO NEGATIVE REGULATION OF KERATINOCYTE DIFFERENTIATION	6.14E-03	1.23E-01	2	MSX2, TP63
GO NEGATIVE REGULATION OF PHOSPHOLIPASE ACTIVITY	6.14E-03	1.23E-01	2	ANXA1, ANXA8L1
GO PHARYNGEAL ARCH ARTERY MORPHOGENESIS	6.14E-03	1.23E-01	2	FOLR1, NOG

GO_POSITIVE_REGULATION_OF_GRANULOCYTE_DIFFERENTIATION	6.14E-03	1.23E-01	2	LEF1, RUNX1
GO_RENAL_VESICLE_FORMATION	6.14E-03	1.23E-01	2	SOX9, WNT4
GO_VENTRICULAR_COMPACT_MYOCARDIUM_MORPHOGENESIS	6.14E-03	1.23E-01	2	LRP2, NOG
GO_POSITIVE_REGULATION_OF_MUSCLE_CONTRACTION	6.15E-03	1.23E-01	4	ADRA1B, GPER1, MYOCD, SPHK1
GO_RETINA_DEVELOPMENT_IN_CAMERA_TYPE_EYE	6.27E-03	1.25E-01	7	CYP1B1, DIO3, DLX1, DLX2, SOX9, TFAP2A, TFAP2B
GO_SMOOTH_MUSCLE_CONTRACTION	6.33E-03	1.26E-01	6	ADRA1B, GPER1, GUCY1A1, MYOCD, SLC8A1, SPHK1
GO_BRANCHING_INVOLVED_IN_MAMMARY_GLAND_DUCT_MORPHOGENESIS	6.35E-03	1.26E-01	3	MSX2, TBX3, WNT4
GO_NEGATIVE_REGULATION_OF_MYOBLAST_DIFFERENTIATION	6.35E-03	1.26E-01	3	IL18, SOX9, TBX3
GO_PURINERGIC_RECEPTOR_ACTIVITY	6.35E-03	1.26E-01	3	GPR87, P2RY2, P2RY6
GO_SUBPALLIUM_DEVELOPMENT	6.35E-03	1.26E-01	3	DLX1, DLX2, INHBA
GO_COCHLEA_DEVELOPMENT	6.61E-03	1.30E-01	4	GATA2, GATA3, GRHL3, SOX9
GO_CRANIAL_NERVE_DEVELOPMENT	6.61E-03	1.30E-01	4	HOXB2, HOXB3, ISL1, TFAP2A
GO_RETINA_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	6.61E-03	1.30E-01	4	DIO3, SOX9, TFAP2A, TFAP2B
GO_SARCOMERE_ORGANIZATION	6.61E-03	1.30E-01	4	ANKRD1, CASQ2, LMOD2, MYLK3
GO TRABECULA MORPHOGENESIS	6.61E-03	1.30E-01	4	HEY1, MSX2, NOG, SLC40A1
GO_CELL_GROWTH	6.79E-03	1.33E-01	15	FLRT3, IGFBP3, IGFBP7, INHBA, LEF1, MSX1, MYOCD, NPPB, POSTN, PPARG, SEMA6D, SOX9, SPHK1, WNT3A, ZEB2
GO_COLUMNAR_CUBOIDAL_EPITHELIAL_CELL_DIFFERENTIATION	6.91E-03	1.35E-01	6	CDX2, DLX3, LEF1, PDX1, TP63, WNT4
GO_CELLULAR_COMPONENT_MORPHOGENESIS	6.92E-03	1.35E-01	28	ACTC1, ANKRD1, ANXA1, CASQ2, CDH10, CNTN4, CSF1R, DLX1, DLX3, EFN1, FLRT3, GATA3, ISL1, LEF1, LMOD2, LRP2, MAP1A, MSX1, MYLK3, NOG, PLXNA2, POSTN, SEMA6D, TACSTD2, UNC5C, VIT, WNT3A, ZEB2
GO_PROTEIN_DIMERIZATION_ACTIVITY	6.99E-03	1.36E-01	32	ABCG2, ACP, ADRA1B, ANXA1, CASQ2, CDH10, CSF1R, DMRTA2, EPAS1, FLRT3, GATA3, GDF6, GREM2, HAND1, HEY1, ID4, INHBA, LPL, MEIS1, NECTIN4, NOG, NR2F2, PDX1, PPARG, PRDM6, PRLR, SLC64A, SOX9, TCF21, TFAP2A, TFAP2B, TWIST1
GO_STEROID_HORMONE_MEDIATED_SIGNALING_PATHWAY	7.05E-03	1.36E-01	8	GPER1, ISL1, LEF1, NR2F2, PPARG, RUNX1, TCF21, TP63
GO_METANEPHRIC_NEPHRON_MORPHOGENESIS	7.09E-03	1.36E-01	3	SOX9, WNT4, WNT9B
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_REGULATOR_REGION_DNA_BINDING	7.09E-03	1.36E-01	3	GATA3, TWIST1, WNT3A
GO_REGULATION_OF_RECEPTOR_BINDING	7.09E-03	1.36E-01	3	GREM2, LEF1, NOG
GO TRABECULA FORMATION	7.09E-03	1.36E-01	3	HEY1, MSX2, SLC40A1
GO_LUNG_MORPHOGENESIS	7.10E-03	1.36E-01	4	NOG, SOX9, TCF21, TNC
GO_POSITIVE_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	7.10E-03	1.36E-01	4	ISL1, LEF1, TWIST1, ZNF703
GO_CYTOKINE_SECRETION	7.13E-03	1.37E-01	9	ANXA1, CD274, CSF1R, GATA3, ITGB6, LPL, POSTN, TWIST1, VTCN1
GO_CAMERA_TYPE_EYE_MORPHOGENESIS	7.21E-03	1.38E-01	6	DIO3, MEIS1, SOX9, TFAP2A, TFAP2B, TWIST1
GO_POSITIVE_REGULATION_OF_HEMOPOIESIS	7.28E-03	1.39E-01	8	ANXA1, CCR1, GATA2, GATA3, IL18, INHBA, LEF1, RUNX1
GO_MULTICELLULAR_ORGANISM_PROCESS	7.34E-03	1.40E-01	9	ARHGAP1, CLIC3, IGFBP7, NR2F2, PAPP4, PRLR, SLC64A, STS, WNT4
GO_MUSCLE_CELL_DEVELOPMENT	7.51E-03	1.43E-01	8	ACTC1, ANKRD1, CASQ2, LMOD2, MYLK3, MYOF, SLC8A1, TBX3
GO_CELL_SURFACE	7.62E-03	1.44E-01	23	ACKR3, AMOT, ANXA1, CACNG4, CCR1, CD274, CDH10, CLSTN2, CSF1R, CSF2RA, ENPEP, FGFBP1, FOLR1, IL1R1, ITGB6, LPL, LRP2, PRLR, VTCN1, WNT3A, WNT4, WNT5B, WNT6
GO_NEGATIVE_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESSES	7.62E-03	1.44E-01	4	ACADL, GPER1, SNAI2, WNT4
GO_POSITIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	7.80E-03	1.45E-01	14	ANKRD1, CD274, CSF1R, GATA3, GPER1, ISL1, LPL, PDX1, POSTN, TCAF2, TP63, TWIST1, VTCN1, WLS
GO_CARDIAC_NEURAL_CRESCENT_CELL_DEVELOPMENT_INVOLVED_IN_OUTFLOW_TRACT_MORPHOGENESIS	7.82E-03	1.45E-01	2	FOLR1, TWIST1
GO_CORNEA_DEVELOPMENT_IN_CAMERA_TYPE_EYE	7.82E-03	1.45E-01	2	WNT6, WNT9B
GO_CRANIAL_SUTURE_MORPHOGENESIS	7.82E-03	1.45E-01	2	MSX2, TWIST1
GO_JUNCTIONAL_SARCOPLASMIC_RETICULUM_MEMBRANE	7.82E-03	1.45E-01	2	CASQ2, JPH2
GO_PARAXIAL_MESODERM_MORPHOGENESIS	7.82E-03	1.45E-01	2	LEF1, WNT3A
GO_PROTEIN GLUTAMINE GAMMA GLUTAMYLTRANSFERASE ACTIVITY	7.82E-03	1.45E-01	2	TGM1, TGM2
GO_REGULATION_OF_CARDIAC_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	7.82E-03	1.45E-01	2	NOG, TWIST1
GO_REGULATION_OF_MALE_GONAD_DEVELOPMENT	7.82E-03	1.45E-01	2	SOX9, WNT4
GO_SECONDARY_HEART_FIELD_SPECIFICATION	7.82E-03	1.45E-01	2	ISL1, LRP2
GO_NEGATIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	7.89E-03	1.46E-01	3	NOG, SNAI2, SOX9
GO_NEGATIVE_REGULATION_OF_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	7.89E-03	1.46E-01	3	ANXA1, CD274, RUNX1
GO_OUTFLOW_TRACT_SEPTUM_MORPHOGENESIS	7.89E-03	1.46E-01	3	ISL1, LRP2, MSX2
GO_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	7.89E-03	1.46E-01	3	ANXA1, IL18, IL1R1
GO_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	7.98E-03	1.47E-01	9	ANXA1, BMPER, EFN1, FGFBP1, GATA2, GATA3, NR2F2, PPARG, PRKD1
GO_CELL_DIFFERENTIATION_IN_SPINAL_CORD	8.16E-03	1.50E-01	4	EVX1, GATA2, ISL1, WNT3A
GO_POSITIVE_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	8.37E-03	1.53E-01	16	ANKRD1, CLSTN2, DLX1, DLX2, DMRTA2, FLRT3, GATA2, GDF6, GPER1, LRP2, PLXNA2, PPARG, PRKD1, WNT3A, ZEB2, ZNF804A
GO_SECOND_MESSENGER_MEDIATED_SIGNALING	8.41E-03	1.54E-01	14	ACKR3, ADGRG1, ADRA1B, CASQ2, CCR1, GPER1, GUCY1A1, JPH2, NPPB, P2RY6, PDX1, SLC8A1, SOX9, SPHK1
GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIIUM_INTO_CYTOSOL	8.46E-03	1.55E-01	5	CASQ2, GPER1, JPH2, P2RY6, SLC8A1
GO_IMPORT_ACROSS_PLASMA_MEMBRANE	8.52E-03	1.55E-01	6	FOLR1, KCNJ13, KCNJ15, LRP2, SLC8A1, TRPV6
GO_RESPONSE_TO_FIBROBLAST_GROWTH_FACTOR	8.68E-03	1.57E-01	7	FGFBP1, FLRT3, GATA3, NOG, POSTN, TNC, WNT4
GO_COLLAGEN_FIBRIL_ORGANIZATION	8.72E-03	1.57E-01	4	COL11A1, COL3A1, CYP1B1, LUM
GO_POSITIVE_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFERATION	8.72E-03	1.57E-01	4	ADGRG1, DMRTA2, LRP2, WNT3A
GO_RNA_POLYMERASE_II_TRANSCRIPTION_FACTOR_BINDING	8.72E-03	1.57E-01	4	ANKRD1, ID4, PITX1, TBX3
GO_CRANIAL_NERVE_MORPHOGENESIS	8.74E-03	1.57E-01	3	HOXB2, HOXB3, TFAP2A
GO_INSULIN-LIKE_GROWTH_FACTOR_BINDING	8.74E-03	1.57E-01	3	HTRA3, IGFBP3, IGFBP7
GO_POSITIVE_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	8.74E-03	1.57E-01	3	GPER1, P2RY6, WNT4
GO_REGULATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE ACTIVITY	9.39E-03	1.69E-01	9	DLX1, GPER1, LEF1, PPARG, SOX7, TFAP2B, TNFSF15, TP63, WNT3A
GO_NEGATIVE_REGULATION_OF_HEMOPOIESIS	9.61E-03	1.72E-01	7	ANXA1, GATA2, HOXB8, INHBA, MEIS1, MEIS2, RUNX1
GO_CARDIAC_MUSCLE_CELL_FATE_COMMITMENT	9.67E-03	1.72E-01	2	TBX3, WNT3A
GO_CELLULAR_RESPONSE_TO_CAFFEINE	9.67E-03	1.72E-01	2	CASQ2, SLC8A1
GO_NOTOCHORD_MORPHOGENESIS	9.67E-03	1.72E-01	2	EFNA1, NOG
GO_POSITIVE_REGULATION_OF KERATINOCYTE PROLIFERATION	9.67E-03	1.72E-01	2	TGM1, TP63
GO_PROSTATIC_BUD_FORMATION	9.67E-03	1.72E-01	2	NOG, TP63
GO_ACTOMYOSIN_STRUCTURE_ORGANIZATION	9.87E-03	1.75E-01	8	ACTC1, ANKRD1, CASQ2, DLX1, LMOD2, MYLK3, TACSTD2, WNT4
GO_HORMONE_MEDIATED_SIGNALING_PATHWAY	9.90E-03	1.75E-01	9	GPER1, ISL1, LEF1, NR2F2, PPARG, PRLR, RUNX1, TCF21, TP63
GO_MORPHOGENESIS_OF_AN_EPITHELIAL_SHEET	9.92E-03	1.75E-01	4	FLRT3, HOXB2, HOXB4, MSX2
GO_POSITIVE_REGULATION_OF_CHEMOKINE_PRODUCTION	9.92E-03	1.75E-01	4	CSF1R, LPL, POSTN, TWIST1
GO_POSITIVE_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACTIVITY	9.92E-03	1.75E-01	4	AFAP1L2, CSF1R, EFN1, WNT3A

Supplemental Table S4. Gene ontology (GO) categories identified as associated (p-value<0.01) with genes expressed at significantly lower expression levels in differentiated vs. undifferentiated hESCs. Gene ontology categories are listed along with their respective p-values of enrichment, false discovery rate (FDR)-adjusted p-values of enrichment, and specific genes relevant to each gene ontology category.

Gene Ontology Category	p-value	FDR-adjusted p-value	Number of Genes with Significantly Lower Expression in Differentiated vs. Undifferentiated hESCs within GO Category	Genes with Significantly Lower Expression in Differentiated vs. Undifferentiated hESCs within GO Category
GO_BEHAVIOR	4.12E-09	4.12E-05	33	ADCY5, ADCY8, ADGRB3, APLN, ARC, BDNF, C1QL1, CACNA1B, CALB1, CPT1A, DMBX1, GABRA5, GAL, GDF15, GPR176, GRIN1, GRPR, JPH4, KCND2, LGH4, MRAP2, NLGN1, NMU, NPW, NPY1R, NRXN2, PAX5, PPP1R1B, PRKCG, RGS14, SLC17A7, SLC24A2, SLC8A2
GO_SYNAPTIC_SIGNALING	3.16E-08	1.58E-04	35	ADCY8, AMPH, ARC, BDNF, CACNA1A, CACNA1B, CACNB4, CACNG7, CALB1, DGKB, GABRA5, GPR176, GRIN1, GRM4, HRH3, JPH4, KCND2, KCNN1, KIF5A, MYCBPAP, NLGN1, NMU, NRG3, NRXN2, PPPIA4, PRKCG, RGS14, SHISA8, SLC17A7, SLC24A2, SLC8A2, SNCB, SYN3, SYT12, UNC13A
GO_NEURON_REMODELING	1.74E-06	5.80E-03	5	ADGRB3, C1QL1, C3, EPHA8, NTN4
GO_CELL_CELL_SIGNALING	3.53E-06	7.81E-03	54	ADCY5, ADCY8, AMPH, APLN, ARC, BDNF, BST2, C3, CACNA1A, CACNA1B, CACNB4, CACNG7, CALB1, CHST4, CPT1A, CXCL5, DGKB, FGF4, FGF8, GABRA5, GAL, GCK, GDF15, GPR176, GRIN1, GRM4, HECW1, HRH3, ITGAM, JPH4, KCND2, KCNN1, KIF5A, MYCBPAP, NLGN1, NMU, NODAL, NRG3, NRXN2, PPPIA4, PRKCG, PSMB8, RGS14, RSPO4, SHISA8, SLC17A7, SLC24A2, SLC8A2, SNCB, SYN3, SYT12, THY1, TRHDE, UNC13A
GO_COGNITION	3.91E-06	7.81E-03	18	ADCY8, ADGRB3, ARC, BDNF, C1QL1, CALB1, GABRA5, GRIN1, GRPR, HRH3, JPH4, NRXN2, PPP1R1B, PRKCG, RGS14, SLC17A7, SLC24A2, SLC8A2
GO_CELL_BODY_MEMBRANE	7.06E-06	1.10E-02	6	ADCY8, ATP1A3, GABRA5, KCND2, THY1, UNC5A
GO_REGULATION_OF_TRANS_SYNAPTIC_SIGNALING	7.67E-06	1.10E-02	22	ADCY8, ARC, BDNF, CACNA1A, CACNA1B, CACNG7, CALB1, DGKB, GRIN1, GRM4, JPH4, NLGN1, NMU, NRG3, PRKCG, RGS14, SHISA8, SLC24A2, SLC8A2, SYN3, SYT12, UNC13A
GO_FEEDING_BEHAVIOR	1.11E-05	1.38E-02	10	APLN, CPT1A, DMBX1, GAL, GDF15, GRIN1, MRAP2, NMU, NPW, NPY1R
GO_SYNAPSE	1.42E-05	1.52E-02	41	ADCY8, ADGRB3, AMPH, ARC, ATCAY, ATP1A3, BDNF, C1QL1, CABP1, CACNA1B, CACNG7, CALB1, CAMKV, CPEB1, DGKB, GABRA5, GRIA4, GRIN1, GRM4, HRH3, KCND2, KIF5A, NLGN1, NMU, NRG3, NRXN2, PPPIA4, PPP1R1B, PRKCG, RASGRP2, RGS14, SEPT3, SEPT4, SHISA8, SLC17A7, SLC8A2, SLITRK3, SNCB, SYN3, SYT12, UNC13A
GO_NEURON_MATURATION	1.53E-05	1.52E-02	7	ADGRB3, C1QL1, C3, EPHA8, LGH4, NTN4, RET
GO_SOMATODENDRITIC_COMPARTMENT	1.67E-05	1.52E-02	32	ADCY2, ADCY8, ARC, ARHGEF15, ATCAY, ATP1A3, BDNF, CACNA1A, CACNA1B, CACNG7, CALB1, CPEB1, GABRA5, GAL, GRIA4, GRIN1, HRH3, JPH4, KCND2, KCNN1, KIF17, KIF21B, KIF5A, NLGN1, PPP1R1B, PRKCG, RET, RGS14, SLC8A2, THY1, TUBB4A, UNC5A
GO_LONG_TERM_MEMORY	1.93E-05	1.59E-02	6	ADCY8, ARC, CALB1, GRIN1, RGS14, SLC17A7
GO_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	2.06E-05	1.59E-02	18	ARC, ATP1B2, CACNB4, CACNG7, FXYD1, FXYD7, GAL, GEM, GRIA4, GRIN1, HECW1, JPH4, KCNH2, MMP9, NLGN1, SHISA8, THY1, TRDN
GO_REGULATION_OF_TRANSPORTER_ACTIVITY	2.41E-05	1.72E-02	16	ARC, ATP1B2, CACNB4, CACNG7, FXYD1, FXYD7, GAL, GEM, GRIA4, GRIN1, HECW1, JPH4, MMP9, NLGN1, SHISA8, TRDN
GO_REGULATION_OF_ION_TRANSMEMBRANE_TRANSPORT	2.71E-05	1.81E-02	22	ARC, ATP1B2, CACNA1A, CACNA1B, CACNB4, CACNG7, FXYD1, FXYD7, GAL, GEM, GRIA4, GRIN1, HECW1, JPH4, KCND2, KCNH2, KCNQ4, MMP9, NLGN1, SHISA8, THY1, TRDN
GO_MEMORY	3.18E-05	1.99E-02	10	ADCY8, ARC, BDNF, CALB1, GRIN1, PPP1R1B, RGS14, SLC17A7, SLC24A2, SLC8A2
GO_SYNAPSE_PART	3.74E-05	2.04E-02	34	ADCY8, ADGRB3, AMPH, ARC, BDNF, C1QL1, CABP1, CACNA1B, CACNG7, CALB1, CPEB1, GABRA5, GRIA4, GRIN1, GRM4, HRH3, KCND2, NLGN1, NMU, NRXN2, PPPIA4, PPP1R1B, PRKCG, RGS14, SEPT3, SEPT4, SHISA8, SLC17A7, SLC8A2, SLITRK3, SNCB, SYN3, SYT12, UNC13A
GO_LEARNING	3.79E-05	2.04E-02	11	ADGRB3, ARC, C1QL1, GABRA5, GRIN1, JPH4, NRXN2, PPP1R1B, RGS14, SLC24A2, SLC8A2
GO_PRESYNAPSE	4.21E-05	2.04E-02	22	ADCY8, AMPH, BDNF, C1QL1, CACNA1B, CALB1, GABRA5, GRIN1, GRM4, HRH3, NLGN1, NMU, NRXN2, PPPIA4, PRKCG, SEPT3, SEPT4, SLC17A7, SNCB, SYN3, SYT12, UNC13A
GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	4.26E-05	2.04E-02	12	ADCY8, ARC, CACNG7, CALB1, GRIN1, NLGN1, NMU, RGS14, SLC24A2, SLC8A2, SYT12, UNC13A
GO_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	4.29E-05	2.04E-02	24	ARC, ATP1B2, C3, CACNA1A, CACNA1B, CACNB4, CACNG7, FGF19, FXYD1, FXYD7, GAL, GEM, GRIA4, GRIN1, HECW1, JPH4, KCND2, KCNH2, KCNQ4, MMP9, NLGN1, SHISA8, THY1, TRDN
GO_CARDIAC_CONDUCTION	4.90E-05	2.23E-02	11	ATP1A3, ATP1B2, ATP2A3, CACNB4, CACNG7, FXYD1, FXYD7, KCND2, KCNH2, SLC8A2, TRDN
GO_CATION_TRANSPORT	5.57E-05	2.35E-02	39	ARC, ATP1A3, ATP1B2, ATP2A3, CACNA1A, CACNA1B, CACNB4, CACNG7, FXYD1, FXYD7, GAL, GCK, GEM, GRIA4, GRIN1, HECW1, HRH3, ICAM1, JPH4, KCND2, KCNH2, KCNN1, KCNQ4, LCK, MAOB, MMP9, NLGN1, PKD1L2, SCNN1B, SHISA8, SLC17A7, SLC24A2, SLC38A4, SLC5A2, SLC6A15, SLC8A2, SYT12, THY1, TRDN
GO_REGULATION_OF_CATION_CHANNEL_ACTIVITY	5.65E-05	2.35E-02	12	ARC, CACNB4, CACNG7, GAL, GEM, GRIA4, GRIN1, JPH4, MMP9, NLGN1, SHISA8, TRDN
GO_REGULATION_OF_ION_TRANSPORT	6.14E-05	2.45E-02	27	ARC, ATP1B2, CACNA1A, CACNA1B, CACNB4, CACNG7, FXYD1, FXYD7, GAL, GCK, GEM, GRIA4, GRIN1, HECW1, HRH3, ICAM1, JPH4, KCND2, KCNH2, KCNQ4, MAOB, MMP9, NLGN1, SHISA8, SYT12, THY1, TRDN
GO_REGULATION_OF_BLOOD_CIRCULATION	7.17E-05	2.76E-02	16	APLN, ATP1A3, ATP1B2, ATP2A3, CACNA1B, CACNB4, CACNG7, FXYD1, FXYD7, ICAM1, KCND2, KCNH2, NMU, SLC8A2, TNN13, TRDN
GO_CATION_TRANSMEMBRANE_TRANSPORT	7.57E-05	2.80E-02	31	ARC, ATP1A3, ATP1B2, ATP2A3, CACNA1A, CACNA1B, CACNB4, CACNG7, FXYD1, FXYD7, GAL, GEM, GRIA4, GRIN1, HECW1, JPH4, KCND2, KCNH2, KCNN1, KCNQ4, LCK, MMP9, NLGN1, PKD1L2, SCNN1B, SHISA8, SLC17A7, SLC24A2, SLC8A2, THY1, TRDN
GO_TRANSPORTER_COMPLEX	8.24E-05	2.81E-02	17	ATP1A3, ATP1B2, CACNA1A, CACNA1B, CACNB4, CACNG7, FXYD1, GABRA5, GRIA4, GRIN1, KCND2, KCNH2, KCNN1, KCNQ4, NLGN1, SCNN1B, SHISA8
GO_REGULATION_OF_SYNAPTIC_PLASTICITY	8.24E-05	2.81E-02	12	ADCY8, ARC, CALB1, GRIN1, JPH4, NLGN1, RGS14, SHISA8, SLC24A2, SLC8A2, SYT12, UNC13A
GO_REGULATION_OF_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	8.60E-05	2.81E-02	7	ARC, CACNG7, GRIA4, GRIN1, NLGN1, SHISA8, UNC13A
GO_CELLULAR_RESPONSE_TO_CALCIUM_ION	8.74E-05	2.81E-02	8	ADCY8, CHP2, CPNE7, DPEP1, NLGN1, RASAL1, RASGRP2, SYT12
GO_METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	9.13E-05	2.81E-02	20	ATP1A3, ATP1B2, ATP2A3, CACNA1A, CACNA1B, CACNB4, CACNG7, GRIN1, JPH4, KCND2, KCNH2, KCNN1, KCNQ4, PKD1L2, SCNN1B, SLC17A7, SLC24A2, SLC5A2, SLC6A15, SLC8A2
GO_SYNAPSE_ORGANIZATION	9.35E-05	2.81E-02	19	ADGRB3, ARC, ARHGEF15, BDNF, C1QL1, C3, CACNB4, CAMKV, DGKB, GRIN1, ITGAM, LINGO2, NLGN1, NRXN2, SEMA4A, SLITRK3, SNCB, THBS2, UNC13A
GO_NEURON_PART	9.57E-05	2.81E-02	51	ADCY2, ADCY8, AMPH, ARC, ARHGEF15, ATCAY, ATP1A3, BDNF, C1QL1, CABP1, CACNA1A, CACNA1B, CACNG7, CALB1, CPEB1, EPHA8, GABRA5, GAL, GRIA4, GRIN1, GRM4, HRH3, JPH4, KCND2, KCNN1, KIF17, KIF21B, KIF5A, MGARP, NLGN1, NMU, NRXN2, PPPIA4, PPP1R1B, PRKCG, RASGRP2, RET, RGS14, SEPT3, SEPT4, SHISA8, SLC17A7, SLC8A2, SLITRK3, SNCB, SYN3, SYT12, THY1, TUBB4A, UNC13A, UNC5A

GO_DENDRITIC_TREE	1.02E-04	2.92E-02	24	ADCY2, ADCY8, ARC, ARHGEF15, ATCAY, BDNF, CACNA1B, CALB1, CPEB1, GRIA4, GRIN1, HHR3, JPH4, KCND2, KIF17, KIF21B, KIF5A, NLGN1, PPP1R1B, PRKCG, RET, RGS14, SLC8A2, THY1
GO_DEVELOPMENTAL_MATURATION	1.10E-04	3.04E-02	15	ADGRB3, ARHGEF15, C1QL1, C3, EPHA8, FAT4, GAL, GRIN1, LGH, NTN4, RET, SEPT4, SLC17A7, SOX8, UNC13A
GO_LONG_TERM_SYNAPTIC_POTENTIATION	1.33E-04	3.52E-02	8	ADCY8, ARC, CALB1, NLGN1, RGS14, SLC24A2, SLC8A2, SYT12
GO_CATION_CHANNEL_COMPLEX	1.34E-04	3.52E-02	13	CACNA1A, CACNA1B, CACNB4, CACNG7, GRIA4, GRIN1, KCND2, KCNH2, KCNN1, KCNQ4, NLGN1, SCN1B, SHISA8
GO_GROWTH_FACTOR_ACTIVITY	1.47E-04	3.77E-02	11	BDNF, FGF19, FGF4, FGF8, GDF15, GDF3, IL34, IL6R, LEFTY1, NODAL, NRG3
GO_CALCIIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVI TY	1.58E-04	3.94E-02	10	ATP2A3, CACNA1A, CACNA1B, CACNB4, CACNG7, GRIN1, JPH4, PKD1L2, SLC24A2, SLC8A2
GO_METAL_ION_TRANSPORT	1.67E-04	4.06E-02	31	ATP1A3, ATP1B2, ATP2A3, CACNA1A, CACNA1B, CACNB4, CACNG7, FXYD1, FXYD7, GAL, GCK, GEM, GRIN1, HECW1, ICAM1, JPH4, KCND2, KCNH2, KCNN1, KCNQ4, LCK, PKD1L2, SCNN1B, SLC17A7, SLC24A2, SLC38A4, SLC5A2, SLC6A15, SLC8A2, THY1, TRDN
GO_HEART_PROCESS	1.95E-04	4.61E-02	15	APLN, ATP1A3, ATP1B2, ATP2A3, CACNA1B, CACNB4, CACNG7, FXYD1, FXYD7, KCND2, KCNH2, NMU, SLC8A2, TNNT3, TRDN
GO_REGULATION_OF_SYNAPSE_STRUCTURE_OR_ACTIVITY	1.98E-04	4.61E-02	13	ADGRB3, ARC, ARHGEF15, BDNF, CAMKV, DGKB, GRIN1, LINGO2, NLGN1, SEMA4A, SLC17A7, SLITRK3, THBS2
GO_POSITIVE_REGULATION_OF_SYNAPSE_ASSEMBLY	2.07E-04	4.70E-02	7	ADGRB3, BDNF, LINGO2, NLGN1, SEMA4A, SLITRK3, THBS2
GO_NEUROTRANSMITTER_TRANSPORT	2.48E-04	5.51E-02	14	APLN, CACNA1B, GRM4, HHR3, MAOB, NLGN1, NRXN2, PPPIA4, PRKCG, SLC17A7, SLC6A15, SYN3, SYT12, UNC13A
GO_REGULATION_OF_CARDIAC_CONDUCTION	2.69E-04	5.85E-02	7	ATP1A3, ATP1B2, ATP2A3, FXYD1, FXYD7, SLC8A2, TRDN
GO_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	2.83E-04	6.02E-02	8	ARC, CACNG7, GRIA4, GRIN1, GRM4, NLGN1, SHISA8, UNC13A
GO_ENDODERM_DEVELOPMENT	2.93E-04	6.10E-02	7	ARC, FGF8, GDF3, MMP9NOG, NODAL, ONECUT1
GO_ION_TRANSMEMBRANE_TRANSPORT	3.60E-04	7.35E-02	36	ADAMTS8, ARC, ATP1A3, ATP1B2, ATP2A3, CACNA1A, CACNA1B, CACNB4, CACNG7, CPT1A, FXYD1, FXYD7, GABRA5, GAL, GEM, GRIA4, GRIN1, HECW1, JPH4, KCND2, KCNH2, KCNN1, KCNQ4, LCK, MMP9, NLGN1, PKD1L2, SCNN1B, SHISA8, SLC17A7, SLC24A2, SLC38A4, SLC6A15, SLC8A2, THY1, TRDN
GO_SIGNALING_RECEPTOR_BINDING	3.89E-04	7.77E-02	47	ACTN3, ADAMTS8, ALKA12, APLN, BDNF, BTN3A1, BTN3A2, BTNL9, C1QL1, C3, CD177, CXCL5, DLL3, DOCK2, FGF19, FGF4, FGF8, FOXH1, GABRA5, GAL, GDF15, GDF3, GRIN1, HCK, HLA-F, ICAM1, ICAM5, IL34, IL6R, KDR, LCK, LEFTY1, MEGF10, MRAP2, NLGN1, NMU, NODAL, NPW, NRG3, NRXN2, NXPH4, PIPOX, PPP1R1B, RSP04, SEMA4A, THY1, TRDN
GO_AMYLOID_BETA_BINDING	4.05E-04	7.95E-02	7	ATP1A3, CACNA1A, CACNA1B, GRIA4, GRIN1, ITGAM, NLGN1
GO_SODIUM_ION_TRANSPORT	4.23E-04	8.12E-02	12	ATP1A3, ATP1B2, FXYD1, FXYD7, HECW1, SCNN1B, SLC17A7, SLC24A2, SLC38A4, SLC5A2, SLC6A15, SLC8A2
GO_CYCLASE_ACTIVITY	5.06E-04	9.19E-02	4	ADCY2, ADCY3, ADCY8, GUCY2C
GO_CYCLIC_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	5.06E-04	9.19E-02	4	ADCY2, ADCY3, ADCY8, GUCY2C
GO_PHOSPHORUS_OXYGEN_LYASE_ACTIVITY	5.06E-04	9.19E-02	4	ADCY2, ADCY3, ADCY8, GUCY2C
GO_ANATOMICAL_STRUCTURE_MATURATION	5.39E-04	9.58E-02	10	ADGRB3, C1QL1, C3, EPHA8, FAT4, GAL, GRIN1, LGH, NTN4, RET
GO_ADENYLATE_CYCLASE_ACTIVITY	5.65E-04	9.58E-02	3	ADCY2, ADCY3, ADCY8
GO_CAMP_BIOSYNTHETIC_PROCESS	5.65E-04	9.58E-02	3	ADCY2, ADCY3, ADCY8
GO_HIGH_VOLTAGE_GATED_CALCIIUM_CHANNEL_ACTIVITY	5.65E-04	9.58E-02	3	CACNA1A, CACNA1B, CACNB4
GO_MEMBRANE_REGION	6.02E-04	1.00E-01	15	ADCY2, ADCY8, ARC, BST2, CD177, FXYD1, HCK, ICAM1, ITGAM, KCND2, KDR, LCK, RET, THY1, UNC5A
GO_NEURON_PROJECTION	6.13E-04	1.00E-01	39	ADCY2, ADCY8, ARC, ARHGEF15, ATCAY, ATP1A3, BDNF, C1QL1, CACNA1B, CACNG7, CALB1, CPEB1, EPHA8, GABRA5, GRIA4, GRIN1, HHR3, JPH4, KCND2, KCNN1, KIF17, KIF21B, KIF5A, MGARP, NLGN1, NMU, PPP1R1B, PRKCG, RASGRP2, RET, RGS14, SEPT3, SHISA8, SLC17A7, SLC8A2, THY1, TUBB4A, UNC13A, UNC5A
GO_REGULATION_OF_SYNAPSE_ASSEMBLY	6.22E-04	1.00E-01	8	ADGRB3, BDNF, GRIN1, LINGO2, NLGN1, SEMA4A, SLITRK3, THBS2
GO_LOCOMOTORY_BEHAVIOR	6.44E-04	1.02E-01	11	ADCY3, ADCY8, C1QL1, CACNA1B, CALB1, DMBX1, GRIN1, KCND2, LGH, NPY1R, PPP1R1B
GO_INORGANIC_ION_TRANSMEMBRANE_TRANSPORT	6.73E-04	1.05E-01	28	ADAMTS8, ATP1A3, ATP1B2, ATP2A3, CACNA1A, CACNA1B, CACNB4, CACNG7, FXYD1, FXYD7, GABRA5, GAL, GEM, GRIN1, HECW1, JPH4, KCND2, KCNH2, KCNN1, KCNQ4, LCK, PKD1L2, SCNN1B, SLC17A7, SLC24A2, SLC8A2, THY1, TRDN
GO_ION_TRANSPORT	6.93E-04	1.06E-01	47	ADAMTS8, ARC, ATP1A3, ATP1B2, ATP2A3, CACNA1A, CACNA1B, CACNB4, CACNG7, CPT1A, FXYD1, FXYD7, GABRA5, GAL, GCK, GEM, GLS2, GRIA4, GRIN1, HECW1, HHR3, ICAM1, JPH4, KCND2, KCNH2, KCNN1, KCNQ4, LCK, MAOB, MMP9, NLGN1, PKD1L2, PPPIA4, SCNN1B, SHISA8, SLC16A14, SLC17A7, SLC24A2, SLC38A4, SLC52A3, SLC5A2, SLC6A15, SLC8A2, SLC05A1, SYT12, THY1, TRDN
GO_REGULATION_OF_CELL_MORPHOGENESIS	7.04E-04	1.06E-01	19	ADGRB3, ARC, BDNF, CACNG7, CDC42EP5, GRIN1, HCK, HECW1, ICAM1, ISLR2, KDR, NEUROG3, NLGN1, RAS4L1, RET, RHOH, SEMA4A, THY1, UNC13A
GO_TRANSMEMBRANE_TRANSPORT	7.14E-04	1.06E-01	45	ABCG4, ADAMTS8, AQP4, ARC, ATP1A3, ATP1B2, ATP2A3, C3, CACNA1A, CACNA1B, CACNB4, CACNG7, CPT1A, FGF19, FXYD1, FXYD7, GABRA5, GAL, GEM, GRIA4, GRIN1, HECW1, JPH4, KCND2, KCNH2, KCNN1, KCNQ4, LCK, MMP9, NLGN1, PKD1L2, PSMB8, SCNN1B, SHISA8, SLC16A14, SLC17A7, SLC17A9, SLC24A2, SLC38A4, SLC5A2, SLC6A15, SLC8A2, SLC05A1, THY1, TRDN
GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	7.21E-04	1.06E-01	9	ATP1A3, ATP1B2, FXYD1, FXYD7, HECW1, SCNN1B, SLC17A7, SLC24A2, SLC8A2
GO_REGULATION_OF_SIGNALING_RECEPTOR_ACTIVITY	7.56E-04	1.10E-01	22	APLN, ARC, BDNF, CACNG7, CXCL5, FGF19, FGF4, FGF8, GAL, GDF15, GDF3, GRIA4, GRIN1, IL34, IL6R, LEFTY1, MRAP2, NLGN1, NODAL, NRG3, SHISA8, ZFYVE28
GO_RESPONSE_TO_FORSKOLIN	7.67E-04	1.10E-01	3	ADCY2, ADCY3, ADCY8
GO_SIGNAL_RELEASE_FROM_SYNAPSE	7.84E-04	1.10E-01	10	CACNA1B, GRM4, HHR3, NLGN1, NRXN2, PPPIA4, PRKCG, SYN3, SYT12, UNC13A
GO_REGULATION_OF_AMPA_RECEPTOR_ACTIVITY	8.40E-04	1.17E-01	4	ARC, CACNG7, NLGN1, SHISA8
GO_MULTICELLULAR_ORGANISMAL_SIGNALING	8.95E-04	1.22E-01	11	ATP1A3, ATP1B2, ATP2A3, CACNB4, CACNG7, FXYD1, FXYD7, KCND2, KCNH2, SLC8A2, TRDN
GO_ADENYLATE_CYCLASE_INHIBITING_G_PROTEIN_COUPLED RECEPTOR_SIGNALING_PATHWAY	8.99E-04	1.22E-01	7	ADCY2, ADCY3, ADCY8, GPR176, GRM4, HHR3, NPY1R
GO_CELL_MATURATION	9.37E-04	1.24E-01	10	ADGRB3, C1QL1, C3, EPHA8, GAL, LGH, NTN4, RET, SEPT4, SOX8
GO_REGULATION_OF_TRANSPORT	9.40E-04	1.24E-01	50	ADCY3, ADCY8, APLN, ARC, ATP1B2, BST2, C3, CABP1, CACNA1A, CACNA1B, CACNB4, CACNG7, CAMK1D, CD177, CHP2, CPT1A, DOCK2, FGF19, FXYD1, FXYD7, GAL, GCK, GEM, GRIA4, GRIN1, HCK, HECW1, HLA-F, HHR3, ICAM1, ITGAM, JPH4, KCND2, KCNH2, KCNQ4, LRAT, MAOB, MAPK11, MMP9, NLGN1, NLRP12, NMU, PRKCG, SEPT4, SHISA8, SLC17A7, SYT12, THY1, TRDN, UNC13A
GO_SODIUM_POTASSIUM_EXCHANGING_ATPASE_COMPLEX	1.01E-03	1.29E-01	3	ATP1A3, ATP1B2, FXYD1
GO_PASSIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.02E-03	1.29E-01	18	AQP4, CACNA1A, CACNA1B, CACNB4, CACNG7, FXYD1, GABRA5, GRIA4, GRIN1, JPH4, KCND2, KCNH2, KCNN1, KCNQ4, PKD1L2, SCNN1B, SLC17A7, SLC24A2
GO_INTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE	1.02E-03	1.29E-01	47	ADCY2, ADCY3, ADCY8, ADGRB3, ATP1A3, ATP1B2, BST2, CACNG7, CD1D, EPHA8, FXYD1, GABRA5, GPR176, GRIA4, GRIN1, GRM4, GRPR, HHR3, ICAM1, ICAM5, IL6R, ITGAM, KCND2, KCNH2, KCNN1, KCNQ4, KDR, NLGN1, NPY1R, NRG3, PROCR, RET, SCNN1B, SEMA4A, SHISA8, SLC16A14, SLC24A2, SLC38A4, SLC52A3, SLC6A15, SLC8A2, SLC05A1, SLITRK3, THY1, TMEM130, TRHDE, UNC5A
GO_INNervation	1.13E-03	1.42E-01	4	GABRA5, PRKCG, RET, UNC13A

GO_SIGNAL_RELEASE	1.18E-03	1.46E-01	18	ADCY5, ADCY8, APLN, CACNA1A, CACNA1B, CPT1A, GAL, GCK, GRM4, HRH3, NLGN1, NMU, NRXN2, PPPIA4, PRKCG, SYN3, SYTI2, UNC13A
GO_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	1.26E-03	1.54E-01	14	ATP2A3, CACNA1A, CACNA1B, CACNB4, CACNG7, GEM, GRIN1, JPH4, LCK, PKD1L2, SLC24A2, SLC8A2, THY1, TRDN
GO_RESPONSE_TO_PLATELET_AGGREGATION_INHIBITOR	1.30E-03	1.56E-01	3	ADCY2, ADCY5, ADCY8
GO_REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	1.34E-03	1.59E-01	6	ARC, CACNG7, GRIA4, GRIN1, NLGN1, SHISA8
GO_POSITIVE_REGULATION_OF_SIGNALING	1.39E-03	1.63E-01	49	ADCY8, ALKAL2, APLN, ARC, BDNF, BST2, C3, CACNG7, CALB1, CHP2, EPHA8, FGF19, FGF4, FGF8, GAL, GCK, GDF15, GDF3, GRIN1, GRM4, ICAM1, IL6R, KDR, LCK, LEFTY1, LMO3, MAPK11, MMP9, MRAP2, NLGN1, NLRCS, NLRP12, NMU, NODAL, PIK3API, PIK3R5, PIM2, PSMB8, RET, RGS14, RSP04, SEPT4, SH2D2A, SH2D3C, SLC24A2, SLC8A2, SYTI2, TRDN, UNC13A
GO_RESPONSE_TO_TYPE_I_INTERFERON	1.40E-03	1.63E-01	7	BST2, C19orf66, HLA-F, IFITM1, ISG15, NLRCS, PSMB8
GO_CATION_CHANNEL_ACTIVITY	1.42E-03	1.63E-01	14	CACNA1A, CACNA1B, CACNB4, CACNG7, GRIA4, GRIN1, JPH4, KCND2, KCNH2, KCNN1, KCNQ4, PKD1L2, SCNN1B, SLC24A2
GO_PLASMA_MEMBRANE_REGION	1.48E-03	1.65E-01	35	ADCY8, AQP4, ARC, ATP1B2, BST2, CABP1, CACNG7, CD177, CD1D, CPEB1, DPEP1, FXYD1, GABRA5, GRIA4, GRIN1, GRM4, HCK, IL6R, ITGAM, KCND2, KCNQ4, KIF17, NLGN1, PRKCG, RASGRP2, RGS14, SCNN1B, SHISA8, SLC52A3, SLC8A2, SLITRK3, SORBS2, THY1, UNC13A, UNC5A
GO_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	1.48E-03	1.65E-01	28	ADAMTS6, ATP1A3, ATP1B2, ATP2A3, CACNA1A, CACNA1B, CACNB4, CACNG7, FXYD1, GABRA5, GRIA4, GRIN1, JPH4, KCND2, KCNH2, KCNN1, KCNQ4, PKD1L2, SCNN1B, SLC6A14, SLC17A7, SLC24A2, SLC38A4, SLC52A3, SLC5A2, SLC6A15, SLC8A2, SLC05A1
GO_CIRCULATORY_SYSTEM_PROCESS	1.49E-03	1.65E-01	20	ADAMTS16, APLN, ATP1A3, ATP1B2, ATP2A3, CACNA1B, CACNB4, CACNG7, FXYD1, FXYD7, HSD11B2, ICAM1, KCND2, KCNH2, KLK1, NMU, NPY1R, SLC8A2, TNNB3, TRDN
GO_REGULATION_OF_SHORT_TERM_NEURONAL_SYNAPTIC_PLASTICITY	1.63E-03	1.74E-01	3	SHISA8, SLC8A2, UNC13A
GO_SODIUM_ION_EXPORT_ACROSS_PLASMA_MEMBRANE	1.63E-03	1.74E-01	3	ATP1A3, ATP1B2, FXYD1
GO_SYNAPTIC_CLEFT	1.63E-03	1.74E-01	3	ADGRB3, C1QL1, GRIN1
GO_MOLECULAR_FUNCTION_REGULATOR	1.64E-03	1.74E-01	48	ADGRB3, ALKAL2, APLN, ARHGEF15, ARHGEF28, ATP1B2, BDNF, BST2, C3, CABP1, CACNG7, CCNA1, CXCL5, DOCK2, DPEP1, ELFN2, FGF19, FGF4, FGF8, FXYD1, FXYD7, GAL, GDF15, GDF3, GEM, IL34, IL6R, LEFTY1, MRAP2, NLRP12, NODAL, NRG3, NRXN2, PIK3R5, PPP1R16B, PPP1R1B, PPP2R2B, RAB31L1, RASAL1, RASGRP2, RGS11, RGS14, RHOH, SEMA4A, SH2D3C, SNCB, THY1, TNNB3
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATHWAY	1.68E-03	1.77E-01	24	APLN, ARHGEF28, BDNF, EPHA8, FAT4, FGF19, FGF4, FGF8, FGFRL1, GDF15, GRIN1, HCK, JAK3, KDR, LCK, MAPK11, MMP9, NRG3, PRDM14, RET, RGS14, SH2D2A, TRIM72, ZFYVE28
GO_NEUROPEPTIDE_RECEPTOR_BINDING	1.70E-03	1.77E-01	4	APLN, GAL, MRAP2, NMU
GO_NEURON_SPINE	1.77E-03	1.83E-01	9	ARC, CALB1, GRIA4, GRIN1, KCND2, NLGN1, PPP1R1B, RGS14, SLC8A2
GO_REGULATION_OF_NEURONAL_SYNAPTIC_PLASTICITY	1.85E-03	1.89E-01	5	ARC, GRIN1, SHISA8, SLC8A2, UNC13A
GO_POSTSYNAPTIC_SPECIALIZATION_MEMBRANE	1.88E-03	1.90E-01	7	ARC, CACNG7, GABRA5, GRIN1, KCND2, NLGN1, SLITRK3
GO_CATION_TRANSPORTING_ATPASE_COMPLEX	2.01E-03	2.01E-01	3	ATP1A3, ATP1B2, FXYD1
GO_RESPONSE_TO_MORPHINE	2.17E-03	2.12E-01	4	ADCY8, GRIN1, PPP1R1B, PRKCG
GO_INTRINSIC_COMPONENT_OF_POSTSYNAPTIC_SPECIALIZATION_MEMBRANE	2.18E-03	2.12E-01	6	CACNG7, GABRA5, GRIN1, KCND2, NLGN1, SLITRK3
GO_NERVE_DEVELOPMENT	2.18E-03	2.12E-01	6	BDNF, GABRA5, HES3, PRKCG, RET, UNC13A
GO_MONOVALENT_INORGANIC_CATION_TRANSPORT	2.22E-03	2.14E-01	19	ATP1A3, ATP1B2, ATP2A3, FXYD1, FXYD7, GAL, GCK, HECW1, KCND2, KCNH2, KCNN1, KCNQ4, SCNN1B, SLC17A7, SLC24A2, SLC38A4, SLC5A2, SLC6A15, SLC8A2
GO_NEUROTRANSMITTER_RECEPTOR_COMPLEX	2.39E-03	2.28E-01	5	CACNG7, GRIA4, GRIN1, NLGN1, SHISA8
GO_NEURON_CELL_CELL_ADHESION	2.44E-03	2.30E-01	3	NLGN1, NRXN2, RET
GO_ENZYME_LINKED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	2.46E-03	2.30E-01	31	APLN, ARHGEF28, BDNF, EPHA8, FAT4, FGF19, FGF4, FGF8, FGFRL1, FOXH1, GDF15, GDF3, GRIN1, GUCY2C, HCK, JAK3, KDR, LCK, LEFTY1, MAPK11, MMP9, NODAL, NRG3, NRXN2, ONECUT1, PRDM14, RET, RGS14, SH2D2A, TRIM72, ZFYVE28
GO_CALCIUM_ION_BINDING	2.54E-03	2.35E-01	23	ACTN3, C1R, CABP1, CACNA1B, CALB1, CALN1, CHP2, DGKB, DLL3, F12, FAT4, GRIN1, MAN1C1, MASPI, PKD1L2, RASGRP2, RET, SNCB, SYTI2, THBS2, TLL2, TUBB4A, UNC13A
GO_GATED_CHANNEL_ACTIVITY	2.63E-03	2.41E-01	14	CACNA1A, CACNA1B, CACNB4, CACNG7, GABRA5, GRIA4, GRIN1, JPH4, KCND2, KCNH2, KCNN1, KCNQ4, SCNN1B, SLC17A7
GO_PROTEIN_LOCALIZATION_TO_SYNAPE	2.65E-03	2.41E-01	6	CACNG7, GRIN1, KIF17, KIF5A, NLGN1, NRXN2
GO_EXPORT_ACROSS_PLASMA_MEMBRANE	2.72E-03	2.43E-01	4	ATP1A3, ATP1B2, FXYD1, KCNH2
GO_NEURON_TO_NEURON_SYNAPE	2.85E-03	2.43E-01	14	ADCY8, ARC, CABP1, CACNG7, CALB1, CPEB1, GRIN1, KCND2, NLGN1, PRKCG, RGS14, SHISA8, SLITRK3, SYN3
GO_ANTEROGRADE_DENDRITIC_TRANSPORT	2.89E-03	2.43E-01	2	KIF17, KIF5A
GO_FORMATION_OF_ANATOMICAL_BOUNDARY	2.89E-03	2.43E-01	2	GDF3, NODAL
GO_MESENCHODERM_DEVELOPMENT	2.89E-03	2.43E-01	2	FGF8, NODAL
GO_MOTOR_LEARNING	2.89E-03	2.43E-01	2	ADGRB3, C1QL1
GO_O PALMITOYLTRANSFERASE_ACTIVITY	2.89E-03	2.43E-01	2	CPT1A, LRAT
GO_POSITIVE_REGULATION_OF_MHC_CLASS_I_BIOSYNTHETIC_PROCESS	2.89E-03	2.43E-01	2	NLRCS, NLRP12
GO_POSITIVE_REGULATION_OF_NEUTROPHIL_ACTIVATION	2.89E-03	2.43E-01	2	CD177, ITGAM
GO_REGULATION_OF_METAL_ION_TRANSPORT	2.94E-03	2.45E-01	15	ATP1B2, CACNA1B, CACNB4, FXYD1, FXYD7, GAL, GCK, GEM, GRIN1, HECW1, ICAM1, JPH4, KCNH2, THY1, TRDN
GO_REGULATION_OF_KIDNEY_DEVELOPMENT	3.04E-03	2.51E-01	5	FAT4, IL6R, MMP9, RET, SOX8
GO_VOLTAGE_GATED_CATION_CHANNEL_ACTIVITY	3.22E-03	2.64E-01	8	CACNA1A, CACNA1B, CACNB4, CACNG7, GRIN1, KCND2, KCNH2, KCNQ4
GO_RENAL_WATER_HOMEOSTASIS	3.37E-03	2.74E-01	4	ADCY2, ADCY5, ADCY8, AQP4
GO_GLUTAMATERGIC_SYNAPE	3.41E-03	2.75E-01	14	ADCY8, ARC, CACNG7, CALB1, CAMKY, DGKB, GRIN1, KCND2, NLGN1, NRG3, PPP1R1B, RGS14, SYN3, UNC13A
GO_ACTIVATION_OF_PROTEIN_KINASE_A_ACTIVITY	3.47E-03	2.77E-01	3	ADCY2, ADCY5, ADCY8
GO_SYNAPTIC_MEMBRANE	3.49E-03	2.77E-01	16	ADCY8, ARC, CABP1, CACNG7, CPEB1, GABRA5, GRIA4, GRIN1, GRM4, KCND2, NLGN1, PRKCG, RGS14, SHISA8, SLITRK3, UNC13A
GO_SYNAPSE_ASSEMBLY	3.81E-03	3.00E-01	9	ADGRB3, BDNF, GRIN1, LINGO2, NLGN1, NRXN2, SEMA4A, SLITRK3, THBS2
GO_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	3.91E-03	3.05E-01	7	APLN, FAT4, FGF19, FGF4, FGF8, FGFRL1, PRDM14
GO_CAMERA_TYPE_EYE_PHOTORECEPTOR_CELL_DIFFERENTIATION	4.07E-03	3.15E-01	3	RORB, SOX8, THY1
GO_LOCALIZATION_WITHIN_MEMBRANE	4.15E-03	3.15E-01	8	ARC, CACNG7, DOCK2, KIF17, KIF5A, NLGN1, NRXN2, THY1
GO_CELL_BODY	4.23E-03	3.15E-01	19	ADCY8, ARC, ATP1A3, CACNA1A, CACNA1B, CACNG7, CALB1, GABRA5, GAL, GRIA4, KCND2, KCNN1, KIF5A, PPP1R1B, RET, SLC8A2, THY1, TUBB4A, UNC5A
GO_POSTSYNAPTIC_MEMBRANE	4.24E-03	3.15E-01	13	ADCY8, ARC, CABP1, CACNG7, CPEB1, GABRA5, GRIA4, GRIN1, KCND2, NLGN1, RGS14, SHISA8, SLITRK3
GO_CELLULAR_RESPONSE_TO_INORGANIC_SUBSTANCE	4.27E-03	3.15E-01	10	ADCY8, CHP2, CPNE7, DPEP1, FBPI1, MMP9, NLGN1, RASAL1, RASGRP2, SYTI2
GO_CEREBELLAR_MOSSY_FIBER	4.29E-03	3.15E-01	2	CACNG7, SLC17A7
GO_MHC_CLASS_I_BIOSYNTHETIC_PROCESS	4.29E-03	3.15E-01	2	NLRCS, NLRP12
GO_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_GROWTH	4.29E-03	3.15E-01	2	ACTN3, TLL2
GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	4.33E-03	3.16E-01	8	ATP1A3, ATP1B2, SCNN1B, SLC17A7, SLC24A2, SLC5A2, SLC6A15, SLC8A2
GO_NEURAL_RETINA_DEVELOPMENT	4.37E-03	3.17E-01	5	CALB1, RORB, SLC17A7, SOX8, THY1

GO_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	4.50E-03	3.18E-01	21	ATPIA3, ATP1B2, ATP2A3, CACNA1A, CACNA1B, CACNB4, CACNG7, GRIA4, GRIN1, JPH4, KCND2, KCNH2, KCNN1, KCNQ4, PKD1L2, SCNN1B, SLC17A7, SLC24A2, SLC5A2, SLC6A15, SLC8A2
GO_RESPONSE_TO_CALCIUM_ION	4.51E-03	3.18E-01	8	ADCY8, CHP2, CPNE7, DPEPI, NLGN1, RASAL1, RASGRP2, SYT12
GO_REGULATION_OF_DENDRITE_MORPHOGENESIS	4.51E-03	3.18E-01	6	ADGRB3, ARC, GRIN1, HECW1, NEUROG3, NLGN1
GO_PALMITOYLTRANSFERASE_ACTIVITY	4.51E-03	3.18E-01	4	CPT1A, LRAT, ZDHHC19, ZDHHC22
GO_COMPLEMENT_BINDING	4.72E-03	3.30E-01	3	CR2, ITGAM, MEGF10
GO_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	4.87E-03	3.38E-01	30	ABCG4, ADAMTS8, AQP4, ATP1A3, ATP1B2, ATP2A3, CACNA1A, CACNA1B, CACNB4, CACNG7, FXYP1, GABRA5, GRIA4, GRIN1, JPH4, KCND2, KCNH2, KCNN1, KCNQ4, PKD1L2, SCNN1B, SLC16A14, SLC17A7, SLC24A2, SLC38A4, SLC52A3, SLC5A2, SLC6A15, SLC8A2, SLC05A1
GO_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	5.01E-03	3.43E-01	27	ADGRB3, ALKAL2, ARC, ARHGEF15, BDNF, CACNG7, CAMK1D, DLL3, GRIN1, HECW1, HES3, ISLR2, LGI4, LINGO2, NEUROG3, NLGN1, NRG3, RASAL1, RET, RGS14, SIPR5, SEMA4A, SLITRK3, SOX8, THBS2, THY1, UNC134
GO_REGULATION_OF_SYSTEM_PROCESS	5.02E-03	3.43E-01	20	ACTN3, APLN, ATP1A3, ATP1B2, ATP2A3, CACNA1B, CACNB4, CACNG7, FXYP1, FXYP7, GAL, GRIN1, ICAM1, KCND2, KCNH2, NLGN1, NMu, SLC8A2, TNNI3, TRDN
GO_POSTSYNAPSE	5.20E-03	3.53E-01	20	ADCY8, ADGRB3, ARC, CABP1, CACNG7, CALB1, CPEB1, GABRA5, GRIA4, GRIN1, KCND2, NLGN1, PPP1R1B, PRKCG, RGS14, SHISA8, SLC17A7, SLC8A2, SLITRK3, SYN3
GO_SYNAPTIC_TRANSMISSION_Glutamatergic	5.30E-03	3.58E-01	6	CACNG7, GRIN1, GRM4, NLGN1, SLC17A7, UNC134
GO_PEPTIDE_BINDING	5.56E-03	3.71E-01	12	ATPIA3, CABP1, CACNA1A, CACNA1B, CD1D, GRIA4, GRIN1, GRPR, HLA-F, ITGAM, NLGN1, TRHDE
GO_PLASMA_MEMBRANE_PROTEIN_COMPLEX	5.58E-03	3.71E-01	19	ATPIA3, ATP1B2, CACNA1A, CACNA1B, CACNB4, CACNG7, FXYP1, GRIA4, GRIN1, HLA-F, IL6R, ITGAM, KCND2, KCNH2, KCNN1, KCNQ4, NLGN1, RET, SHISA8
GO_REGULATION_OF_NEUROTRANSMITTER_LEVELS	5.60E-03	3.71E-01	13	CACNA1B, GRM4, HHRH3, ICAM1, MAOB, NLGN1, NRXN2, PPFI4, PRKCG, SLC17A7, SYN3, SYT12, UNC134
GO_NEGATIVE_REGULATION_OF_ION_TRANSPORT	5.70E-03	3.71E-01	8	GEM, HECW1, HHRH3, ICAM1, KCNH2, MAOB, MMP9, TRDN
GO_AXIAL_MESODERM_DEVELOPMENT	5.93E-03	3.71E-01	2	FOXH1, NODAL
GO_BETA_2_MICROGLOBULIN_BINDING	5.93E-03	3.71E-01	2	CD1D, HLA-F
GO_GPI_ANCHOR_BINDING	5.93E-03	3.71E-01	2	DPEPI, THY1
GO_JUNCTIONAL_MEMBRANE_COMPLEX	5.93E-03	3.71E-01	2	JPH4, TRDN
GO_NEGATIVE_REGULATION_OF_CELLULAR_AMINE_METABOLIC_PROCESS	5.93E-03	3.71E-01	2	ATCAY, ITGAM
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_MEMBRANE_POTENTIAL	5.93E-03	3.71E-01	2	FXYP1, TRDN
GO_REGULATION_OF_SEROTONIN_SECRETION	5.93E-03	3.71E-01	2	HRH3, MAOB
GO_T_CELL_RECEPTOR_BINDING	5.93E-03	3.71E-01	2	DOCK2, LCK
GO_ATPASE_DEPENDENT_TRANSMEMBRANE_TRANSPORT_COMPLEX	6.22E-03	3.86E-01	3	ATPIA3, ATP1B2, FXYP1
GO_RHYTHMIC_BEHAVIOR	6.42E-03	3.94E-01	4	GPR176, KCND2, NLGN1, NMu
GO_VOLTAGE_GATED_CALCIUM_CHANNEL_COMPLEX	6.42E-03	3.94E-01	4	CACNA1A, CACNA1B, CACNB4, CACNG7
GO_INTEGRIN_BINDING	6.70E-03	4.08E-01	7	ACTN3, ADAMTS8, CD177, ICAM1, ICAM5, KDR, THY1
GO_Glutamate_SECRETION	6.97E-03	4.20E-01	4	GLS2, HHRH3, PPFI4, SLC17A7
GO_METANEPHRIC_NEPHRON_EPITHELIUM_DEVELOPMENT	7.06E-03	4.20E-01	3	CALB1, FAT4, SOX8
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DEGRANULATION	7.06E-03	4.20E-01	3	CD177, HLA-F, ITGAM
GO_REGULATION_OF_RESPIRATORY_GASEOUS_EXCHANGE	7.06E-03	4.20E-01	3	APLN, GRIN1, NLGN1
GO_REGULATION_OF_DEVELOPMENTAL_GROWTH	7.28E-03	4.28E-01	13	ACTN3, BDNF, CACNG7, FGF8, GAL, GDF15, ISLR2, MAPK11, NPY1R, RASAL1, SEMA4A, TLL2, UNC13A
GO_CELL_PART_MORPHOGENESIS	7.30E-03	4.28E-01	21	ADGRB3, ARC, BDNF, CACNG7, EPHA8, FGF8, GRIN1, HECW1, ISLR2, KIF54, NEUROG3, NLGN1, NTN4, RASAL1, RET, SEMA4A, SLITRK3, SPON2, THY1, UNC13A, UNC5A
GO_WATER_HOMEOSTASIS	7.32E-03	4.28E-01	5	ADCY2, ADCY5, ADCY8, AQP4, SCNN1B
GO_PROTEIN_TRANSPORT_WITHIN_PLASMA_MEMBRANE	7.54E-03	4.38E-01	4	ARC, CACNG7, KIF17, KIF54
GO_PROTEIN_TYROSINE_KINASE_ACTIVITY	7.58E-03	4.38E-01	7	EPHA8, FGFR1, HCK, JAK3, KDR, LCK, RET
GO_CALMODULIN_BINDING	7.81E-03	4.42E-01	9	ADCY8, CAMK1D, CAMKV, GEM, GRIN1, KCNN1, KCNQ4, SLC8A2, UNC134
GO_DETERMINATION_OF_LEFT_RIGHT_ASYMMETRY_IN_LATE_RAL_MESODERM	7.82E-03	4.42E-01	2	FOXH1, NODAL
GO_REGULATION_OF_NEUTROPHIL_DEGRANULATION	7.82E-03	4.42E-01	2	CD177, ITGAM
GO_SKELETAL_MUSCLE_TISSUE_GROWTH	7.82E-03	4.42E-01	2	ACTN3, TLL2
GO_CALYX_OF_HOLD	7.97E-03	4.42E-01	3	CALB1, PRKCG, UNC13A
GO_CELL_COMMUNICATION_BY_ELECTRICAL_COUPLING_INVOLVED_IN_CARDIAC_CONDUCTION	7.97E-03	4.42E-01	3	ATPIA3, ATP1B2, TRDN
GO_REGULATION_OF_DENDRITE_EXTENSION	7.97E-03	4.42E-01	3	CACNG7, RASAL1, UNC13A
GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	8.06E-03	4.45E-01	9	ARC, ATP1B2, C3, FGF19, FXYP1, GAL, KCNH2, THY1, TRDN
GO_RESPONSE_TO_AMYLOID_BETA	8.15E-03	4.48E-01	4	ATPIA3, CACNA1A, CACNA1B, ICAM1
GO_MESONEPHROS_DEVELOPMENT	8.67E-03	4.74E-01	6	ADAMTS16, CALB1, FAT4, FGF8, RET, SOX8
GO_CALCIUM_CHANNEL_REGULATOR_ACTIVITY	8.79E-03	4.77E-01	4	CACNG7, GEM, NRXN2, TNNI3
GO_EXCITATORY_SYNAPSE_ASSEMBLY	8.94E-03	4.80E-01	3	NLGN1, NRXN2, SEMA4A
GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	8.94E-03	4.80E-01	3	BST2, HLA-F, JAK3
GO_POTASSIUM_ION_TRANSPORT	9.06E-03	4.82E-01	10	ATPIA3, ATP1B2, FXYP1, GAL, GCK, KCND2, KCNH2, KCNN1, KCNQ4, SLC24A2
GO_NEURON_DEVELOPMENT	9.08E-03	4.82E-01	30	ADGRB3, ALKAL2, ARC, ATCAY, BDNF, C1QL1, C3, CACNG7, CAMK1D, EPHA8, FAT4, FGF8, GABRA5, GRIN1, HECW1, ISLR2, KIF5A, LGI4, NEUROG3, NLGN1, NTN4, RASAL1, RET, RORR, SEMA4A, SLITRK3, SPON2, THY1, UNC13A, UNC5A
GO_VESICLE_MEDIATED_TRANSPORT_IN_SYNAPSE	9.12E-03	4.82E-01	9	AMPH, ARC, KIF5A, NLGN1, PRKCG, SLC17A7, SNCB, SYT12, UNC13A
GO_DIVALENT_INORGANIC_CATION_TRANSPORT	9.19E-03	4.84E-01	16	ATP2A3, CACNA1A, CACNA1B, CACNB4, CACNG7, GCK, GEM, GRIN1, ICAM1, JPH4, LCK, PKD1L2, SLC24A2, SLC8A2, THY1, TRDN
GO_POSITIVE_REGULATION_OF_PATHWAY_RESTRICTED_SMA_D_PROTEIN_PHOSPHORYLATION	9.46E-03	4.93E-01	4	GDF15, GDF3, LEFTY1, NODAL
GO_VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	9.46E-03	4.93E-01	4	CACNA1A, CACNA1B, CACNB4, CACNG7
GO_PERIPHERAL_NERVOUS_SYSTEM_DEVELOPMENT	9.73E-03	4.94E-01	5	BDNF, LGI4, NEUROG3, POL3F1, SOX8
GO_NEUROPEPTIDE_SIGNALING_PATHWAY	9.93E-03	4.94E-01	6	GAL, GRPR, NMu, NPW, NPY1R, NXP4
GO_DENDRITIC_TRANSPORT	9.94E-03	4.94E-01	2	KIF17, KIF5A
GO_GLIAL_CELL_DERIVED_NEUROTROPHIC_FACTOR_RECEPTOR_SIGNALING_PATHWAY	9.94E-03	4.94E-01	2	GDF15, RET
GO_JUNCTIONAL_SARCOPLASMIC_RETICULUM_MEMBRANE	9.94E-03	4.94E-01	2	JPH4, TRDN
GO_MIDBRAIN_HINDBRAIN_BOUNDARY_DEVELOPMENT	9.94E-03	4.94E-01	2	FGF8, HES3
GO_POSTSYNAPTIC_DENSITY_PROTEIN_95_CLUSTERING	9.94E-03	4.94E-01	2	NLGN1, NRXN2
GO_CELLULAR_RESPONSE_TO_GLUcAGON_STIMULUS	9.98E-03	4.94E-01	3	ADCY2, ADCY5, ADCY8
GO_DOPAMINE_METABOLIC_PROCESS	9.98E-03	4.94E-01	3	ITGAM, MAOB, SNCB
GO_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_BINDING	9.98E-03	4.94E-01	3	FGF19, FGF4, FGF8

[illegible]

[illegible]

[illegible]

[illegible]

Supplemental Table S5. Genes identified with significantly altered expression levels in placenta-derived TS cells (CT30 and CT29) vs hPSC-TS cells (H1 and H9). A total of 110 genes are listed here that show a false discovery rate (FDR) $q\text{-value} < 0.05$ (based on ANOVA p-values) and fold change (FC) ≥ 1.5 or (FC) ≤ -1.5 (calculated as the ratio of the average across all placenta-derived TS samples over the average across all hPSC-TS samples).

EnsembleID	GeneSymbol	p-value	FDR q-value	FC (placenta-derived TS/ hPSC-TS)
ENSG00000198300	<i>PEG3</i>	2.93E-09	1.51E-06	2.61
ENSG00000127399	<i>LRRC61</i>	1.16E-08	4.43E-06	2.50
ENSG00000238222	<i>MKRN4P</i>	9.91E-15	4.93E-11	2.33
ENSG00000156269	<i>NAA11</i>	3.24E-08	9.50E-06	2.15
ENSG00000273018	<i>AC107983.2</i>	3.27E-11	2.81E-08	2.13
ENSG00000154874	<i>CCDC144B</i>	1.97E-11	1.96E-08	2.12
ENSG00000146833	<i>TRIM4</i>	1.59E-06	1.59E-04	2.07
ENSG00000224597	<i>SVIL-AS1</i>	2.61E-16	1.95E-12	2.06
ENSG00000188707	<i>ZBED6CL</i>	8.09E-09	3.33E-06	2.05
ENSG00000234444	<i>ZNF736</i>	1.79E-07	3.51E-05	1.99
ENSG00000187600	<i>AC016912.1</i>	3.11E-09	1.55E-06	1.98
ENSG00000279377	<i>AC003973.3</i>	7.04E-07	9.48E-05	1.95
ENSG00000100181	<i>TPTEP1</i>	5.35E-05	1.54E-03	1.93
ENSG00000223518	<i>CSNK1A1P1</i>	3.38E-11	2.81E-08	1.86
ENSG00000187581	<i>COX8C</i>	5.71E-06	3.84E-04	1.86
ENSG00000283633	<i>AP000547.3</i>	3.55E-05	1.19E-03	1.84
ENSG00000154898	<i>CCDC144CP</i>	4.29E-12	7.12E-09	1.79
ENSG00000139567	<i>ACVRL1</i>	1.34E-05	6.66E-04	1.76
ENSG00000189423	<i>USP32P3</i>	3.46E-12	6.45E-09	1.74
ENSG00000154997	<i>SEPT14</i>	5.22E-05	1.51E-03	1.72
ENSG00000189223	<i>PAX8-AS1</i>	6.49E-05	1.71E-03	1.71
ENSG00000134539	<i>KLRD1</i>	9.88E-12	1.23E-08	1.70
ENSG00000154027	<i>AK5</i>	2.89E-11	2.70E-08	1.70
ENSG00000134757	<i>DSG3</i>	9.19E-05	2.11E-03	1.69
ENSG00000213077	<i>NA</i>	5.34E-13	1.33E-09	1.68
ENSG00000254101	<i>LINC02055</i>	7.51E-08	1.70E-05	1.68
ENSG00000206075	<i>SERPINB5</i>	7.31E-05	1.82E-03	1.67
ENSG00000100628	<i>ASB2</i>	3.13E-07	5.30E-05	1.67
ENSG00000229676	<i>ZNF492</i>	3.10E-05	1.10E-03	1.66
ENSG00000274286	<i>ADRA2B</i>	4.10E-07	6.58E-05	1.65
ENSG00000270533	<i>CR382285.1</i>	3.64E-06	2.64E-04	1.64
ENSG00000197083	<i>ZNF300P1</i>	2.88E-06	2.29E-04	1.63
ENSG00000120669	<i>SOHLH2</i>	9.59E-07	1.20E-04	1.62
ENSG00000120279	<i>MYCT1</i>	1.10E-06	1.27E-04	1.61

ENSG00000233913	<i>RPL10P9</i>	7.53E-03	3.46E-02	1.60
ENSG00000215146	<i>BX322639.1</i>	1.30E-04	2.61E-03	1.60
ENSG00000228100	<i>LINC01820</i>	5.61E-08	1.35E-05	1.59
ENSG00000115828	<i>QPCT</i>	4.17E-05	1.32E-03	1.59
ENSG00000233327	<i>USP32P2</i>	2.19E-10	1.56E-07	1.59
ENSG00000184571	<i>PIWIL3</i>	9.29E-04	9.04E-03	1.58
ENSG00000137948	<i>BRDT</i>	2.51E-03	1.72E-02	1.58
ENSG00000182050	<i>MGAT4C</i>	1.15E-06	1.31E-04	1.58
ENSG00000166897	<i>ELFN2</i>	2.33E-09	1.39E-06	1.58
ENSG00000204644	<i>ZFP57</i>	7.26E-04	7.69E-03	1.58
ENSG00000261143	<i>ADAMTS7P3</i>	3.32E-05	1.15E-03	1.57
ENSG00000260518	<i>BMS1P8</i>	5.87E-05	1.62E-03	1.57
ENSG00000187627	<i>RGPD1</i>	3.41E-07	5.60E-05	1.57
ENSG00000218739	<i>CEBPZOS</i>	2.71E-04	4.18E-03	1.56
ENSG00000213115	<i>AC104131.1</i>	2.76E-05	1.02E-03	1.56
ENSG00000138161	<i>CUZD1</i>	1.86E-08	6.62E-06	1.55
ENSG00000125618	<i>PAX8</i>	7.82E-05	1.91E-03	1.54
ENSG00000198542	<i>ITGBL1</i>	3.97E-08	1.07E-05	1.54
ENSG00000248685	<i>LINC02484</i>	1.58E-05	7.30E-04	1.54
ENSG00000163623	<i>NKX6-1</i>	1.21E-09	7.87E-07	1.53
ENSG00000255642	<i>PABPC1P4</i>	2.19E-07	4.01E-05	1.52
ENSG00000234787	<i>LINC00458</i>	5.49E-04	6.46E-03	1.52
ENSG00000066827	<i>ZFAT</i>	1.87E-16	1.95E-12	1.52
ENSG00000258484	<i>SPESP1</i>	1.08E-02	4.28E-02	1.52
ENSG00000240241	<i>AC108752.1</i>	1.06E-03	9.92E-03	1.52
ENSG00000213225	<i>NOC2LP1</i>	2.38E-04	3.85E-03	1.51
ENSG00000011028	<i>MRC2</i>	1.15E-04	2.41E-03	1.50
ENSG00000086288	<i>NME8</i>	1.55E-05	7.28E-04	-1.50
ENSG00000250616	<i>AC012645.1</i>	2.14E-03	1.56E-02	-1.50
ENSG00000145247	<i>OCIAD2</i>	1.16E-05	6.04E-04	-1.51
ENSG00000257151	<i>PWAR6</i>	1.03E-02	4.16E-02	-1.52
ENSG00000175806	<i>MSRA</i>	7.60E-04	7.92E-03	-1.52
ENSG00000269981	<i>AL627309.7</i>	5.64E-07	8.17E-05	-1.52
ENSG00000268903	<i>AL627309.6</i>	4.74E-08	1.22E-05	-1.53
ENSG00000185885	<i>IFITM1</i>	1.15E-04	2.41E-03	-1.53
ENSG00000196581	<i>AJAP1</i>	1.34E-04	2.67E-03	-1.53
ENSG00000196507	<i>TCEAL3</i>	6.42E-04	7.10E-03	-1.53
ENSG00000121898	<i>CPXM2</i>	2.27E-04	3.73E-03	-1.54
ENSG00000112541	<i>PDE10A</i>	2.31E-04	3.77E-03	-1.54
ENSG00000187630	<i>DHRS4L2</i>	2.07E-06	1.93E-04	-1.54
ENSG00000104059	<i>FAM189A1</i>	3.24E-04	4.68E-03	-1.55

ENSG00000081842	<i>PCDHA6</i>	2.87E-04	4.36E-03	-1.56
ENSG00000154760	<i>SLFN13</i>	5.14E-05	1.51E-03	-1.57
ENSG00000189023	<i>MAGEB16</i>	2.41E-03	1.68E-02	-1.57
ENSG00000264070	<i>DND1P1</i>	6.07E-14	1.81E-10	-1.57
ENSG00000171045	<i>TSNARE1</i>	8.25E-09	3.33E-06	-1.57
ENSG00000165338	<i>HECTD2</i>	9.32E-04	9.05E-03	-1.58
ENSG00000224078	<i>SNHG14</i>	3.72E-03	2.19E-02	-1.58
ENSG00000141255	<i>SPATA22</i>	2.09E-03	1.53E-02	-1.59
ENSG00000128739	<i>SNRPN</i>	3.84E-03	2.24E-02	-1.59
ENSG00000173068	<i>BNC2</i>	1.17E-03	1.06E-02	-1.60
ENSG00000248383	<i>PCDHAC1</i>	1.08E-04	2.32E-03	-1.60
ENSG00000276345	<i>AC004556.1</i>	1.03E-02	4.17E-02	-1.60
ENSG00000262539	<i>AC005829.2</i>	1.29E-11	1.48E-08	-1.60
ENSG00000105501	<i>SIGLEC5</i>	4.22E-04	5.48E-03	-1.63
ENSG00000204969	<i>PCDHA2</i>	6.52E-05	1.71E-03	-1.65
ENSG00000103227	<i>LMF1</i>	3.23E-06	2.44E-04	-1.66
ENSG00000225532	<i>AL731684.1</i>	7.15E-05	1.81E-03	-1.66
ENSG00000133687	<i>TMTC1</i>	1.07E-02	4.27E-02	-1.66
ENSG00000118523	<i>CTGF</i>	5.07E-04	6.14E-03	-1.67
ENSG00000227766	<i>HCG4P5</i>	1.65E-05	7.54E-04	-1.71
ENSG00000185201	<i>IFITM2</i>	1.07E-03	9.94E-03	-1.73
ENSG00000157326	<i>DHRS4</i>	5.45E-08	1.35E-05	-1.74
ENSG00000150433	<i>TMEM218</i>	4.32E-04	5.54E-03	-1.75
ENSG00000112852	<i>PCDHB2</i>	3.66E-05	1.21E-03	-1.76
ENSG00000213025	<i>COX20P1</i>	2.21E-12	4.71E-09	-1.76
ENSG00000258498	<i>DIO3OS</i>	1.19E-02	4.57E-02	-1.79
ENSG00000204967	<i>PCDHA4</i>	6.00E-06	3.95E-04	-1.81
ENSG00000044459	<i>CNTLN</i>	4.90E-04	6.01E-03	-1.85
ENSG00000176769	<i>TCERG1L</i>	2.91E-09	1.51E-06	-1.86
ENSG00000249158	<i>PCDHA11</i>	6.38E-05	1.69E-03	-1.88
ENSG00000254415	<i>SIGLEC14</i>	9.10E-05	2.10E-03	-1.90
ENSG00000250120	<i>PCDHA10</i>	6.66E-07	9.06E-05	-2.01
ENSG00000251664	<i>PCDHA12</i>	1.01E-06	1.23E-04	-2.16
ENSG00000197406	<i>DIO3</i>	5.33E-03	2.76E-02	-2.25
ENSG00000170430	<i>MGMT</i>	1.93E-14	7.21E-11	-2.40

Supplemental Table S7. Genes identified with significantly higher expression levels in hPSC-TS^{CDX2} vs. hPSC-TS cells. A total of 269 genes are listed here that show a false discovery rate (FDR) q-value<0.05 (based on ANOVA p-values) and fold change (FC) ≥ 1.5 (calculated as the ratio of the average across all hPSC-TS^{CDX2} samples over the average across all hPSC-TS samples).

EnsembleID	GeneSymbol	p-value	FDR q-value	FC (hTESCs / hTSCs)
ENSG00000117152	<i>RGS4</i>	1.24E-07	3.32E-06	2.77
ENSG00000164616	<i>FBXL21</i>	1.30E-10	6.20E-08	2.74
ENSG00000139219	<i>COL2A1</i>	6.42E-11	4.62E-08	2.52
ENSG00000145826	<i>LECT2</i>	1.39E-12	4.16E-09	2.49
ENSG00000107562	<i>CXCL12</i>	1.30E-07	3.38E-06	2.44
ENSG00000121361	<i>KCNJ8</i>	3.95E-05	1.90E-04	2.25
ENSG00000233101	<i>HOXB-AS3</i>	2.35E-08	1.23E-06	2.19
ENSG00000170689	<i>HOXB9</i>	5.06E-05	2.27E-04	2.18
ENSG00000110975	<i>SYT10</i>	5.44E-07	8.65E-06	2.17
ENSG00000170961	<i>HAS2</i>	1.17E-06	1.46E-05	2.15
ENSG00000156113	<i>KCNMA1</i>	2.43E-06	2.50E-05	2.14
ENSG00000164649	<i>CDCA7L</i>	2.07E-09	3.20E-07	2.14
ENSG00000176887	<i>SOX11</i>	7.06E-08	2.32E-06	2.13
ENSG00000008196	<i>TFAP2B</i>	1.05E-07	3.04E-06	2.12
ENSG00000138795	<i>LEF1</i>	2.68E-06	2.69E-05	2.11
ENSG00000140807	<i>NKD1</i>	7.36E-10	1.52E-07	2.11
ENSG00000120068	<i>HOXB8</i>	1.51E-06	1.77E-05	2.10
ENSG00000183463	<i>URAD</i>	5.81E-11	4.62E-08	2.09
ENSG00000078018	<i>MAP2</i>	9.94E-06	7.09E-05	2.05
ENSG00000206579	<i>XKR4</i>	2.18E-08	1.17E-06	2.05
ENSG00000182168	<i>UNC5C</i>	6.47E-06	5.16E-05	2.05
ENSG00000037965	<i>HOXC8</i>	3.03E-10	9.35E-08	2.05
ENSG00000183454	<i>GRIN2A</i>	1.58E-08	9.42E-07	2.04
ENSG00000087116	<i>ADAMTS2</i>	2.14E-05	1.21E-04	2.04
ENSG00000099284	<i>H2AFY2</i>	1.08E-07	3.09E-06	2.04
ENSG00000101825	<i>MXRA5</i>	1.42E-05	9.16E-05	2.03
ENSG00000159387	<i>IRX6</i>	6.17E-08	2.16E-06	2.03
ENSG00000154864	<i>PIEZO2</i>	3.34E-04	9.49E-04	2.02
ENSG00000266074	<i>BAHCC1</i>	5.93E-10	1.30E-07	2.02
ENSG00000196628	<i>TCF4</i>	3.82E-08	1.62E-06	2.02
ENSG00000165556	<i>CDX2</i>	6.68E-09	6.17E-07	2.01
ENSG00000143248	<i>RGS5</i>	2.60E-07	5.37E-06	2.00
ENSG00000169439	<i>SDC2</i>	5.65E-07	8.89E-06	1.99
ENSG00000111186	<i>WNT5B</i>	3.85E-07	6.94E-06	1.98
ENSG00000177508	<i>IRX3</i>	8.37E-05	3.34E-04	1.98
ENSG00000164116	<i>GUCY1A1</i>	9.75E-05	3.75E-04	1.98
ENSG00000170579	<i>DLGAP1</i>	1.59E-11	2.38E-08	1.98
ENSG00000137573	<i>SULF1</i>	3.75E-05	1.82E-04	1.98
ENSG00000121440	<i>PDZRN3</i>	7.27E-07	1.06E-05	1.97
ENSG00000016082	<i>ISL1</i>	2.79E-07	5.59E-06	1.97
ENSG00000145147	<i>SLIT2</i>	5.77E-06	4.71E-05	1.97
ENSG00000156466	<i>GDF6</i>	1.82E-09	2.90E-07	1.97
ENSG00000157657	<i>ZNF618</i>	6.64E-08	2.24E-06	1.96
ENSG00000149256	<i>TENM4</i>	3.30E-05	1.67E-04	1.95
ENSG00000123901	<i>GPR83</i>	7.66E-09	6.40E-07	1.95
ENSG00000106804	<i>C5</i>	5.57E-09	5.62E-07	1.95

ENSG00000105880	<i>DLX5</i>	3.67E-07	6.68E-06	1.94
ENSG00000172201	<i>ID4</i>	1.03E-08	7.37E-07	1.94
ENSG00000120075	<i>HOXB5</i>	5.75E-10	1.28E-07	1.94
ENSG00000108511	<i>HOXB6</i>	1.07E-08	7.52E-07	1.93
ENSG00000041982	<i>TNC</i>	1.10E-04	4.11E-04	1.92
ENSG00000164161	<i>HHIP</i>	5.47E-06	4.52E-05	1.92
ENSG00000189056	<i>RELN</i>	2.08E-04	6.63E-04	1.92
ENSG00000145824	<i>CXCL14</i>	2.38E-05	1.31E-04	1.91
ENSG00000160801	<i>PTH1R</i>	4.93E-08	1.91E-06	1.90
ENSG00000162706	<i>CADM3</i>	8.51E-06	6.35E-05	1.89
ENSG00000253641	<i>AC104964.1</i>	5.36E-07	8.60E-06	1.89
ENSG00000111962	<i>UST</i>	6.36E-06	5.09E-05	1.89
ENSG00000237515	<i>SHISA9</i>	4.02E-07	7.16E-06	1.89
ENSG00000276644	<i>DACH1</i>	2.14E-04	6.77E-04	1.88
ENSG00000253649	<i>PRSS51</i>	1.97E-06	2.15E-05	1.88
ENSG00000198795	<i>ZNF521</i>	4.76E-06	4.06E-05	1.88
ENSG00000165023	<i>DIRAS2</i>	2.51E-09	3.51E-07	1.88
ENSG00000272505	<i>AC104964.4</i>	3.57E-06	3.33E-05	1.88
ENSG00000130294	<i>KIF1A</i>	2.04E-03	3.76E-03	1.88
ENSG00000270885	<i>RASL10B</i>	2.12E-07	4.62E-06	1.87
ENSG00000204103	<i>MAFB</i>	6.72E-08	2.24E-06	1.87
ENSG00000144619	<i>CNTN4</i>	1.95E-06	2.13E-05	1.87
ENSG00000140945	<i>CDH13</i>	1.39E-04	4.90E-04	1.87
ENSG00000162493	<i>PDPN</i>	7.26E-07	1.06E-05	1.86
ENSG00000154856	<i>APCDD1</i>	1.02E-07	2.98E-06	1.85
ENSG00000171243	<i>SOSTDC1</i>	3.91E-06	3.52E-05	1.84
ENSG00000107796	<i>ACTA2</i>	7.33E-06	5.66E-05	1.83
ENSG00000094755	<i>GABRP</i>	4.54E-04	1.19E-03	1.83
ENSG00000198732	<i>SMOC1</i>	1.89E-02	2.14E-02	1.83
ENSG00000188488	<i>SERPINA5</i>	3.02E-03	5.09E-03	1.82
ENSG00000156475	<i>PPP2R2B</i>	5.93E-05	2.56E-04	1.82
ENSG00000019505	<i>SYT13</i>	2.17E-04	6.85E-04	1.82
ENSG00000133110	<i>POSTN</i>	1.40E-03	2.81E-03	1.82
ENSG00000248690	<i>HAS2-AS1</i>	5.44E-07	8.65E-06	1.81
ENSG00000197859	<i>ADAMTSL2</i>	5.67E-06	4.65E-05	1.81
ENSG00000185565	<i>LSAMP</i>	1.68E-04	5.65E-04	1.80
ENSG00000135547	<i>HEY2</i>	2.76E-07	5.55E-06	1.80
ENSG00000224940	<i>PRRT4</i>	2.25E-05	1.26E-04	1.80
ENSG00000140873	<i>ADAMTS18</i>	7.04E-06	5.49E-05	1.79
ENSG00000060718	<i>COL11A1</i>	6.49E-04	1.56E-03	1.79
ENSG00000148468	<i>FAM171A1</i>	5.17E-06	4.32E-05	1.79
ENSG00000107105	<i>ELAVL2</i>	1.08E-03	2.30E-03	1.78
ENSG00000228412	<i>AL022068.1</i>	2.23E-06	2.34E-05	1.77
ENSG00000078687	<i>TNRC6C</i>	2.71E-06	2.71E-05	1.77
ENSG00000250305	<i>TRMT9B</i>	1.48E-07	3.63E-06	1.77
ENSG00000168542	<i>COL3A1</i>	5.18E-04	1.32E-03	1.76
ENSG00000071575	<i>TRIB2</i>	2.95E-05	1.54E-04	1.76
ENSG00000053328	<i>METTL24</i>	1.75E-05	1.05E-04	1.76
ENSG00000163359	<i>COL6A3</i>	1.31E-03	2.66E-03	1.76
ENSG00000279692	<i>AC110285.7</i>	7.48E-09	6.33E-07	1.76
ENSG00000234224	<i>TMEM229A</i>	5.39E-06	4.47E-05	1.76
ENSG00000169851	<i>PCDH7</i>	2.92E-04	8.59E-04	1.75

ENSG00000107731	<i>UNC5B</i>	2.62E-08	1.30E-06	1.75
ENSG00000158966	<i>CACHD1</i>	2.70E-07	5.47E-06	1.75
ENSG00000177096	<i>FAM109B</i>	1.95E-11	2.38E-08	1.75
ENSG00000138134	<i>STAMBPL1</i>	3.54E-08	1.53E-06	1.75
ENSG00000134986	<i>NREP</i>	1.39E-05	9.00E-05	1.75
ENSG00000259663	<i>AC010478.1</i>	1.05E-07	3.04E-06	1.75
ENSG00000245694	<i>CRNDE</i>	7.12E-08	2.32E-06	1.74
ENSG00000082293	<i>COL19A1</i>	1.14E-05	7.75E-05	1.74
ENSG00000146674	<i>IGFBP3</i>	4.19E-04	1.12E-03	1.74
ENSG00000145808	<i>ADAMTS19</i>	5.15E-05	2.31E-04	1.74
ENSG00000164764	<i>SBSPON</i>	6.35E-08	2.19E-06	1.74
ENSG00000065675	<i>PRKCQ</i>	3.00E-06	2.92E-05	1.74
ENSG00000152270	<i>PDE3B</i>	9.38E-06	6.81E-05	1.74
ENSG00000271474	<i>AC106881.1</i>	2.23E-08	1.17E-06	1.74
ENSG00000164484	<i>TMEM200A</i>	1.34E-05	8.78E-05	1.74
ENSG00000126010	<i>GRPR</i>	2.26E-04	7.07E-04	1.74
ENSG00000109472	<i>CPE</i>	4.27E-05	2.01E-04	1.73
ENSG00000148204	<i>CRB2</i>	1.70E-05	1.03E-04	1.72
ENSG00000158321	<i>AUTS2</i>	1.30E-06	1.59E-05	1.72
ENSG00000136859	<i>ANGPTL2</i>	7.82E-07	1.13E-05	1.72
ENSG00000088882	<i>CPXM1</i>	7.70E-07	1.12E-05	1.72
ENSG00000102230	<i>PCYT1B</i>	2.34E-05	1.29E-04	1.72
ENSG00000154783	<i>FGD5</i>	1.46E-03	2.89E-03	1.72
ENSG00000229425	<i>AJ009632.2</i>	8.81E-07	1.22E-05	1.72
ENSG00000172478	<i>C2orf54</i>	3.33E-08	1.47E-06	1.71
ENSG00000128594	<i>LRRC4</i>	1.68E-05	1.03E-04	1.71
ENSG00000160963	<i>COL26A1</i>	5.53E-08	2.04E-06	1.71
ENSG00000157654	<i>PALM2-AKAP2</i>	5.12E-08	1.95E-06	1.71
ENSG00000107295	<i>SH3GL2</i>	1.51E-03	2.98E-03	1.71
ENSG00000081189	<i>MEF2C</i>	1.06E-04	4.01E-04	1.71
ENSG00000188803	<i>SHISA6</i>	1.65E-04	5.57E-04	1.71
ENSG00000064309	<i>CDON</i>	8.86E-09	6.89E-07	1.71
ENSG00000144857	<i>BOC</i>	1.40E-08	8.90E-07	1.70
ENSG00000176641	<i>RNF152</i>	1.08E-04	4.06E-04	1.70
ENSG00000139364	<i>TMEM132B</i>	2.40E-06	2.47E-05	1.70
ENSG00000127578	<i>WFIKKN1</i>	6.05E-06	4.89E-05	1.70
ENSG00000238178	<i>AC078993.1</i>	5.94E-04	1.46E-03	1.70
ENSG00000165449	<i>SLC16A9</i>	5.46E-04	1.37E-03	1.69
ENSG00000280511	<i>AL591030.1</i>	4.78E-05	2.18E-04	1.69
ENSG00000166741	<i>NNMT</i>	4.07E-04	1.10E-03	1.69
ENSG00000198353	<i>HOXC4</i>	3.72E-06	3.41E-05	1.69
ENSG00000145721	<i>LIX1</i>	7.28E-05	3.00E-04	1.69
ENSG00000153993	<i>SEMA3D</i>	2.68E-05	1.43E-04	1.68
ENSG00000206384	<i>COL6A6</i>	8.51E-05	3.39E-04	1.68
ENSG00000248890	<i>HHIP-AS1</i>	1.45E-07	3.61E-06	1.68
ENSG00000137473	<i>TTC29</i>	1.24E-02	1.54E-02	1.68
ENSG00000150551	<i>LYPD1</i>	1.41E-02	1.71E-02	1.67
ENSG00000165379	<i>LRFN5</i>	2.73E-04	8.15E-04	1.67
ENSG00000100078	<i>PLA2G3</i>	1.89E-07	4.25E-06	1.67
ENSG00000254535	<i>PABPC4L</i>	8.64E-08	2.64E-06	1.67
ENSG00000180999	<i>C1orf105</i>	3.37E-08	1.47E-06	1.67
ENSG00000113657	<i>DPYSL3</i>	3.78E-04	1.05E-03	1.67

ENSG00000170374	<i>SP7</i>	2.28E-07	4.87E-06	1.67
ENSG00000235649	<i>MXRA5Y</i>	1.58E-05	9.85E-05	1.67
ENSG00000128656	<i>CHN1</i>	1.01E-06	1.33E-05	1.66
ENSG00000147027	<i>TMEM47</i>	5.31E-05	2.36E-04	1.66
ENSG00000113209	<i>PCDHB5</i>	1.04E-04	3.93E-04	1.66
ENSG00000136732	<i>GYPC</i>	7.04E-04	1.66E-03	1.66
ENSG00000185652	<i>NTF3</i>	3.01E-07	5.81E-06	1.66
ENSG00000183580	<i>FBXL7</i>	1.10E-03	2.34E-03	1.66
ENSG00000177519	<i>RPRM</i>	1.70E-04	5.70E-04	1.66
ENSG00000280623	<i>PCAT14</i>	1.09E-05	7.48E-05	1.66
ENSG00000118785	<i>SPP1</i>	2.71E-03	4.69E-03	1.65
ENSG00000143416	<i>SELENBP1</i>	6.60E-11	4.62E-08	1.65
ENSG00000113722	<i>CDX1</i>	1.70E-04	5.70E-04	1.65
ENSG00000064655	<i>EYA2</i>	4.62E-06	3.99E-05	1.64
ENSG00000274588	<i>DGKK</i>	2.90E-07	5.70E-06	1.64
ENSG00000165125	<i>TRPV6</i>	8.13E-08	2.54E-06	1.64
ENSG00000079102	<i>RUNX1T1</i>	7.79E-06	5.90E-05	1.64
ENSG00000148677	<i>ANKRD1</i>	1.62E-04	5.50E-04	1.64
ENSG00000112137	<i>PHACTR1</i>	5.66E-07	8.89E-06	1.64
ENSG00000163568	<i>AIM2</i>	4.33E-08	1.74E-06	1.64
ENSG00000113749	<i>HRH2</i>	5.30E-08	1.98E-06	1.64
ENSG00000113248	<i>PCDHB15</i>	2.60E-04	7.86E-04	1.63
ENSG00000260597	<i>AC012531.1</i>	4.18E-07	7.33E-06	1.63
ENSG00000121966	<i>CXCR4</i>	2.76E-06	2.74E-05	1.63
ENSG00000172116	<i>CD8B</i>	4.44E-05	2.06E-04	1.63
ENSG00000226956	<i>AP000432.1</i>	3.54E-03	5.78E-03	1.63
ENSG00000184005	<i>ST6GALNAC3</i>	1.50E-04	5.19E-04	1.62
ENSG00000185070	<i>FLRT2</i>	3.43E-03	5.63E-03	1.62
ENSG00000255690	<i>TRIL</i>	3.44E-07	6.40E-06	1.62
ENSG00000226846	<i>LINC00348</i>	2.46E-03	4.34E-03	1.62
ENSG00000175445	<i>LPL</i>	7.89E-05	3.19E-04	1.62
ENSG00000066032	<i>CTNNA2</i>	2.21E-05	1.24E-04	1.62
ENSG00000184731	<i>FAM110C</i>	6.64E-06	5.24E-05	1.62
ENSG00000275585	<i>AC241377.2</i>	1.67E-07	3.88E-06	1.62
ENSG00000048740	<i>CELF2</i>	1.78E-03	3.37E-03	1.62
ENSG00000198121	<i>LPAR1</i>	6.28E-05	2.68E-04	1.61
ENSG00000166863	<i>TAC3</i>	1.65E-06	1.90E-05	1.61
ENSG00000019485	<i>PRDM11</i>	1.96E-07	4.37E-06	1.61
ENSG00000151617	<i>EDNRA</i>	2.88E-03	4.91E-03	1.61
ENSG00000149948	<i>HMG42</i>	1.20E-04	4.38E-04	1.61
ENSG00000146250	<i>PRSS35</i>	3.65E-07	6.66E-06	1.61
ENSG00000227300	<i>KRT16P2</i>	8.29E-03	1.13E-02	1.60
ENSG00000185847	<i>LINC01405</i>	9.80E-07	1.31E-05	1.60
ENSG00000144227	<i>NXPH2</i>	2.17E-05	1.22E-04	1.59
ENSG00000140937	<i>CDH11</i>	2.16E-02	2.38E-02	1.59
ENSG00000223865	<i>HLA-DPB1</i>	2.21E-06	2.33E-05	1.59
ENSG00000135083	<i>CCNJL</i>	1.14E-06	1.45E-05	1.59
ENSG00000160808	<i>MYL3</i>	5.03E-09	5.18E-07	1.59
ENSG00000231918	<i>AC007402.1</i>	7.46E-04	1.73E-03	1.59
ENSG00000081248	<i>CACNA1S</i>	1.54E-04	5.30E-04	1.58
ENSG00000172164	<i>SNTB1</i>	8.41E-05	3.35E-04	1.58
ENSG00000165617	<i>DACT1</i>	1.72E-05	1.04E-04	1.58

ENSG00000185052	<i>SLC24A3</i>	4.69E-07	7.91E-06	1.58
ENSG00000134531	<i>EMPI</i>	1.72E-03	3.28E-03	1.58
ENSG00000177182	<i>CLVS1</i>	9.73E-05	3.75E-04	1.58
ENSG00000144278	<i>GALNT13</i>	3.62E-04	1.01E-03	1.58
ENSG00000158560	<i>DYNC111</i>	1.47E-05	9.34E-05	1.58
ENSG00000185269	<i>NOTUM</i>	4.70E-08	1.84E-06	1.58
ENSG00000138061	<i>CYP1B1</i>	6.06E-05	2.61E-04	1.58
ENSG00000198848	<i>CES1</i>	2.36E-03	4.21E-03	1.57
ENSG00000115844	<i>DLX2</i>	1.12E-06	1.43E-05	1.57
ENSG00000144218	<i>AFF3</i>	1.28E-04	4.59E-04	1.57
ENSG00000165863	<i>C10orf82</i>	3.20E-05	1.63E-04	1.57
ENSG00000178538	<i>CA8</i>	1.00E-05	7.13E-05	1.56
ENSG00000198075	<i>SULT1C4</i>	5.28E-04	1.34E-03	1.56
ENSG00000137642	<i>SORL1</i>	5.56E-05	2.44E-04	1.56
ENSG00000248124	<i>RRN3P1</i>	6.52E-05	2.76E-04	1.56
ENSG00000152931	<i>PART1</i>	6.65E-08	2.24E-06	1.56
ENSG00000069431	<i>ABCC9</i>	9.50E-04	2.09E-03	1.55
ENSG00000145934	<i>TENM2</i>	1.01E-02	1.32E-02	1.55
ENSG00000082556	<i>OPRK1</i>	1.27E-04	4.57E-04	1.55
ENSG00000268555	<i>AC123912.4</i>	5.55E-05	2.44E-04	1.55
ENSG00000093072	<i>ADA2</i>	1.42E-04	4.99E-04	1.55
ENSG00000183098	<i>GPC6</i>	3.37E-04	9.56E-04	1.55
ENSG00000214856	<i>KRT16P1</i>	1.67E-03	3.21E-03	1.55
ENSG00000265174	<i>AP005202.1</i>	6.71E-07	1.01E-05	1.55
ENSG00000102760	<i>RGCC</i>	2.84E-07	5.63E-06	1.55
ENSG00000144642	<i>RBMS3</i>	1.80E-05	1.07E-04	1.55
ENSG00000143502	<i>SUSD4</i>	1.68E-04	5.65E-04	1.54
ENSG00000249421	<i>ADAMTS19-AS1</i>	1.41E-04	4.96E-04	1.54
ENSG00000117707	<i>PROX1</i>	1.65E-07	3.88E-06	1.54
ENSG00000250742	<i>LINC02381</i>	5.50E-05	2.42E-04	1.54
ENSG00000169297	<i>NR0B1</i>	3.36E-04	9.52E-04	1.54
ENSG00000255240	<i>AP001636.3</i>	1.81E-03	3.41E-03	1.53
ENSG00000149451	<i>ADAM33</i>	6.65E-05	2.81E-04	1.53
ENSG00000134532	<i>SOX5</i>	6.04E-04	1.47E-03	1.53
ENSG00000132561	<i>MATN2</i>	4.99E-06	4.20E-05	1.53
ENSG00000187260	<i>WDR86</i>	2.65E-06	2.66E-05	1.53
ENSG00000104324	<i>CPQ</i>	1.37E-04	4.85E-04	1.53
ENSG00000197301	<i>AC090673.1</i>	8.80E-07	1.22E-05	1.53
ENSG00000151632	<i>AKR1C2</i>	4.68E-05	2.15E-04	1.53
ENSG00000072657	<i>TRHDE</i>	3.68E-03	5.96E-03	1.53
ENSG00000172292	<i>CERS6</i>	2.32E-03	4.16E-03	1.53
ENSG00000150556	<i>LYPD6B</i>	2.21E-04	6.94E-04	1.53
ENSG00000239713	<i>APOBEC3G</i>	1.58E-03	3.08E-03	1.53
ENSG00000144792	<i>ZNF660</i>	1.27E-04	4.57E-04	1.53
ENSG00000189184	<i>PCDH18</i>	1.61E-05	9.99E-05	1.53
ENSG00000153885	<i>KCTD15</i>	3.85E-06	3.49E-05	1.53
ENSG00000164946	<i>FREM1</i>	2.64E-05	1.41E-04	1.53
ENSG00000228065	<i>LINC01515</i>	3.20E-06	3.07E-05	1.53
ENSG00000137834	<i>SMAD6</i>	1.61E-07	3.84E-06	1.52
ENSG00000158816	<i>VWA5B1</i>	2.89E-05	1.51E-04	1.52
ENSG00000164879	<i>CA3</i>	1.50E-05	9.50E-05	1.52
ENSG00000131711	<i>MAP1B</i>	3.71E-03	6.01E-03	1.52

ENSG00000158856	<i>DMTN</i>	9.51E-07	1.27E-05	1.52
ENSG00000169554	<i>ZEB2</i>	2.28E-02	2.48E-02	1.51
ENSG00000204291	<i>COL15A1</i>	7.02E-07	1.04E-05	1.51
ENSG00000014257	<i>ACPP</i>	1.82E-04	5.98E-04	1.51
ENSG00000178573	<i>MAF</i>	1.33E-03	2.69E-03	1.51
ENSG00000160191	<i>PDE9A</i>	3.01E-05	1.56E-04	1.51
ENSG00000081138	<i>CDH7</i>	3.27E-04	9.35E-04	1.51
ENSG00000172575	<i>RASGRP1</i>	2.44E-08	1.26E-06	1.51
ENSG00000171291	<i>ZNF439</i>	1.99E-04	6.39E-04	1.51
ENSG00000183853	<i>KIRREL1</i>	3.34E-04	9.49E-04	1.51
ENSG00000180801	<i>ARSJ</i>	3.20E-02	3.21E-02	1.51
ENSG00000237943	<i>PRKCQ-AS1</i>	1.12E-05	7.62E-05	1.50
ENSG00000173376	<i>NDNF</i>	2.85E-03	4.87E-03	1.50
ENSG00000149970	<i>CNKSR2</i>	7.12E-05	2.95E-04	1.50
ENSG00000146021	<i>KLHL3</i>	1.69E-08	9.89E-07	1.50

Supplemental Table S6. Genes identified with significantly altered expression levels in H1 hPSC-TS vs H9 hPSC-TS cells. A total of 109 genes are listed here that show a false discovery rate (FDR) q-value < 0.05 (based on ANOVA p-values) and fold change (FC) ≥ 1.5 or (FC) ≤ -1.5 (calculated as the ratio of the average across all H1 hPSC-TS samples over the average across all H9 hPSC-TS samples).

EnsembleID	GeneSymbol	p-value	FDR q-value	FC (H1 hPSC-TS / H9 hPSC-TS)
ENSG00000129824	<i>RPS4Y1</i>	1.82E-08	3.58E-05	3.07
ENSG00000067048	<i>DDX3Y</i>	2.38E-08	4.00E-05	3.06
ENSG00000114374	<i>USP9Y</i>	4.33E-08	5.41E-05	2.97
ENSG00000131002	<i>TXLNGY</i>	2.52E-08	4.00E-05	2.95
ENSG00000012817	<i>KDM5D</i>	4.21E-09	1.84E-05	2.89
ENSG00000198692	<i>EIF1AY</i>	1.84E-08	3.58E-05	2.64
ENSG00000067646	<i>ZFY</i>	3.91E-09	1.84E-05	2.59
ENSG00000183878	<i>UTY</i>	1.09E-08	3.58E-05	2.56
ENSG00000165246	<i>NLGN4Y</i>	5.76E-04	3.70E-02	2.49
ENSG00000099725	<i>PRKY</i>	2.74E-08	4.00E-05	2.41
ENSG00000233864	<i>TTY15</i>	2.08E-07	2.03E-04	2.40
ENSG00000234449	<i>FAM239A</i>	1.80E-10	3.15E-06	2.28
ENSG00000206159	<i>GYG2P1</i>	3.89E-04	3.07E-02	2.19
ENSG00000159176	<i>CSRP1</i>	1.89E-06	1.07E-03	2.17
ENSG00000226278	<i>PSPHP1</i>	7.09E-07	4.78E-04	2.17
ENSG00000241859	<i>ANOS2P</i>	6.55E-10	5.74E-06	2.15
ENSG00000154620	<i>TMSB4Y</i>	8.88E-03	1.25E-01	2.13
ENSG00000205663	<i>FAM239B</i>	3.68E-07	2.81E-04	2.08
ENSG00000196263	<i>ZNF471</i>	1.07E-03	4.96E-02	1.89
ENSG00000173578	<i>XCRI</i>	1.86E-02	1.67E-01	1.86
ENSG00000205662	<i>FAM239C</i>	2.41E-06	1.32E-03	1.85
ENSG00000258602	<i>LINC01629</i>	2.93E-04	2.59E-02	1.78
ENSG00000176728	<i>TTY14</i>	4.06E-03	9.08E-02	1.77
ENSG00000240241	<i>AC108752.1</i>	1.18E-02	1.40E-01	1.72
ENSG00000092969	<i>TGFB2</i>	4.53E-02	2.21E-01	1.70
ENSG00000234665	<i>AL512625.3</i>	3.27E-08	4.41E-05	1.70
ENSG00000183230	<i>CTNNA3</i>	1.59E-02	1.55E-01	1.68
ENSG00000249321	<i>OR5H5P</i>	1.41E-02	1.49E-01	1.68
ENSG00000221923	<i>ZNF880</i>	4.25E-04	3.18E-02	1.66
ENSG00000146858	<i>ZC3HAV1L</i>	3.81E-03	8.89E-02	1.66
ENSG00000218739	<i>CEBPZOS</i>	2.32E-02	1.80E-01	1.63
ENSG00000234787	<i>LINC00458</i>	6.94E-03	1.11E-01	1.62
ENSG00000166770	<i>ZNF667-AS1</i>	3.14E-02	1.96E-01	1.60
ENSG00000229153	<i>EPHA1-AS1</i>	7.06E-04	4.04E-02	1.60
ENSG00000254122	<i>PCDHGB7</i>	4.78E-03	9.82E-02	1.60
ENSG00000278530	<i>CHMP1B2P</i>	6.41E-04	3.88E-02	1.57
ENSG00000231535	<i>LINC00278</i>	3.57E-05	7.96E-03	1.57
ENSG00000118473	<i>SGIP1</i>	6.63E-03	1.10E-01	1.57

ENSG00000144583	<i>MARCH4</i>	2.69E-02	1.88E-01	1.56
ENSG00000187726	<i>DNAJB13</i>	2.86E-04	2.58E-02	1.55
ENSG00000259884	<i>AC025259.3</i>	2.40E-02	1.83E-01	1.54
ENSG00000255847	<i>AP003717.1</i>	1.41E-05	4.33E-03	1.54
ENSG00000266852	<i>MIR4482</i>	1.11E-04	1.64E-02	1.51
ENSG00000101076	<i>HNF4A</i>	8.92E-04	4.52E-02	-1.50
ENSG00000170085	<i>SIMC1</i>	6.75E-03	1.10E-01	-1.51
ENSG00000070601	<i>FRMPD1</i>	3.66E-03	8.76E-02	-1.51
ENSG00000142173	<i>COL6A2</i>	1.60E-03	6.08E-02	-1.51
ENSG00000165863	<i>C10orf82</i>	5.67E-03	1.04E-01	-1.51
ENSG00000175894	<i>TSPEAR</i>	1.59E-03	6.06E-02	-1.51
ENSG00000236393	<i>AC091806.1</i>	9.73E-03	1.30E-01	-1.52
ENSG00000235890	<i>TSPEAR-AS1</i>	1.07E-04	1.63E-02	-1.52
ENSG00000130303	<i>BST2</i>	2.02E-03	6.75E-02	-1.53
ENSG00000232386	<i>AC015712.1</i>	2.52E-05	6.30E-03	-1.53
ENSG00000053918	<i>KCNQ1</i>	2.38E-03	7.23E-02	-1.54
ENSG00000203783	<i>PRR9</i>	5.77E-03	1.05E-01	-1.54
ENSG00000233922	<i>LINC01694</i>	1.61E-03	6.09E-02	-1.55
ENSG00000244675	<i>AC108676.1</i>	1.16E-03	5.12E-02	-1.56
ENSG00000188002	<i>AC026412.1</i>	1.14E-02	1.39E-01	-1.56
ENSG00000117228	<i>GBP1</i>	1.12E-03	5.04E-02	-1.56
ENSG00000152214	<i>RIT2</i>	3.17E-02	1.96E-01	-1.57
ENSG00000248334	<i>WHAMMP2</i>	8.34E-04	4.43E-02	-1.57
ENSG00000204264	<i>PSMB8</i>	1.82E-03	6.50E-02	-1.57
ENSG00000237846	<i>AL773545.3</i>	5.42E-05	1.04E-02	-1.57
ENSG00000240184	<i>PCDHGC3</i>	4.30E-02	2.17E-01	-1.57
ENSG00000101282	<i>RSPO4</i>	3.93E-03	8.97E-02	-1.58
ENSG00000159674	<i>SPON2</i>	1.15E-02	1.39E-01	-1.60
ENSG00000175040	<i>CHST2</i>	3.64E-04	2.95E-02	-1.60
ENSG00000182912	<i>TSPEAR-AS2</i>	6.62E-04	3.96E-02	-1.61
ENSG00000276805	<i>AL133216.2</i>	5.08E-06	2.07E-03	-1.62
ENSG00000184571	<i>PIWIL3</i>	2.24E-02	1.77E-01	-1.63
ENSG00000172716	<i>SLFN11</i>	3.01E-02	1.94E-01	-1.65
ENSG00000228709	<i>LINC02575</i>	1.10E-04	1.64E-02	-1.66
ENSG00000259676	<i>AC103982.1</i>	7.18E-04	4.05E-02	-1.67
ENSG00000185686	<i>PRAME</i>	1.29E-03	5.47E-02	-1.67
ENSG00000104888	<i>SLC17A7</i>	9.16E-04	4.58E-02	-1.67
ENSG00000050628	<i>PTGER3</i>	2.46E-03	7.32E-02	-1.69
ENSG00000129990	<i>SYT5</i>	6.57E-03	1.09E-01	-1.70
ENSG00000159247	<i>TUBBP5</i>	4.01E-07	2.93E-04	-1.70
ENSG00000129991	<i>TNNI3</i>	4.12E-04	3.10E-02	-1.72
ENSG00000180818	<i>HOXC10</i>	1.54E-02	1.54E-01	-1.72
ENSG00000046774	<i>MAGEC2</i>	3.21E-02	1.98E-01	-1.73
ENSG00000142185	<i>TRPM2</i>	5.30E-03	1.02E-01	-1.73
ENSG00000146038	<i>DCDC2</i>	1.76E-04	1.99E-02	-1.73

ENSG00000204792	<i>LINC01291</i>	5.81E-06	2.26E-03	-1.75
ENSG00000101443	<i>WFDC2</i>	4.84E-03	9.84E-02	-1.75
ENSG00000180938	<i>ZNF572</i>	1.46E-05	4.35E-03	-1.75
ENSG00000105143	<i>SLC1A6</i>	3.62E-03	8.74E-02	-1.77
ENSG00000196436	<i>NPIP15</i>	1.08E-07	1.12E-04	-1.77
ENSG00000130600	<i>HI9</i>	1.55E-03	6.00E-02	-1.80
ENSG00000215030	<i>RPL13P12</i>	5.99E-08	7.00E-05	-1.82
ENSG00000198502	<i>HLA-DRB5</i>	2.57E-06	1.32E-03	-1.84
ENSG00000198105	<i>ZNF248</i>	1.10E-03	5.02E-02	-1.85
ENSG00000197582	<i>GPX1P1</i>	1.55E-06	9.36E-04	-1.89
ENSG00000175161	<i>CADM2</i>	4.63E-05	9.57E-03	-1.95
ENSG00000157766	<i>ACAN</i>	3.18E-04	2.73E-02	-1.95
ENSG00000099251	<i>HSD17B7P2</i>	7.55E-06	2.76E-03	-1.96
ENSG00000180543	<i>TSPYL5</i>	3.72E-03	8.85E-02	-1.97
ENSG00000276345	<i>AC004556.1</i>	3.61E-06	1.54E-03	-1.98
ENSG00000101280	<i>ANGPT4</i>	8.66E-04	4.47E-02	-1.99
ENSG00000269526	<i>ERVV-1</i>	1.64E-04	1.97E-02	-2.01
ENSG00000267943	<i>AC010328.1</i>	7.98E-05	1.37E-02	-2.02
ENSG00000089127	<i>OAS1</i>	1.25E-05	3.91E-03	-2.03
ENSG00000157601	<i>MX1</i>	1.69E-04	1.97E-02	-2.16
ENSG00000111331	<i>OAS3</i>	2.55E-07	2.15E-04	-2.22
ENSG00000236397	<i>DDX11L2</i>	3.10E-07	2.47E-04	-2.25
ENSG00000132321	<i>IQCA1</i>	8.34E-08	9.13E-05	-2.35
ENSG00000179344	<i>HLA-DQB1</i>	3.47E-06	1.52E-03	-2.38
ENSG00000196126	<i>HLA-DRB1</i>	2.57E-07	2.15E-04	-2.39
ENSG00000268964	<i>ERVV-2</i>	6.57E-06	2.45E-03	-2.40

Supplemental Table S8. Genes identified with significantly lower expression levels in hPSC-TS^{CDX2} s vs. hPSC-TS cells. A total of 275 genes are listed here that show a false discovery rate (FDR) q-value<0.05 (based on ANOVA p-values) and fold change (FC) $\leq$ -1.5 (calculated as the ratio of the average across all hPSC-TS^{CDX2} samples over the average across all hPSC-TS samples).

EnsembleID	GeneSymbol	p-value	FDR q-value	FC (hTESCs / hTSCs)
ENSG00000179913	<i>B3GNT3</i>	4.68E-14	4.92E-10	-2.59
ENSG00000280109	<i>PLAC4</i>	1.01E-06	1.32E-05	-2.31
ENSG00000204632	<i>HLA-G</i>	3.45E-10	9.91E-08	-2.26
ENSG00000254415	<i>SIGLEC14</i>	7.73E-07	1.12E-05	-2.24
ENSG00000171303	<i>KCNK3</i>	8.01E-07	1.14E-05	-2.19
ENSG00000174697	<i>LEP</i>	6.10E-05	2.63E-04	-2.14
ENSG00000170627	<i>GTSF1</i>	1.49E-03	2.93E-03	-2.11
ENSG00000213401	<i>MAGEA12</i>	5.78E-04	1.43E-03	-2.11
ENSG00000142511	<i>GPR32</i>	9.83E-07	1.31E-05	-2.07
ENSG00000221867	<i>MAGEA3</i>	1.66E-03	3.19E-03	-2.06
ENSG00000106689	<i>LHX2</i>	5.32E-10	1.24E-07	-2.02
ENSG00000125462	<i>Clorf61</i>	7.07E-13	3.71E-09	-2.01
ENSG00000102287	<i>GABRE</i>	9.91E-08	2.92E-06	-1.98
ENSG00000263711	<i>AC079062.1</i>	4.16E-04	1.12E-03	-1.98
ENSG00000132026	<i>RTBDN</i>	3.23E-10	9.70E-08	-1.98
ENSG00000105501	<i>SIGLEC5</i>	1.33E-11	2.32E-08	-1.97
ENSG00000181126	<i>HLA-V</i>	2.59E-10	9.01E-08	-1.96
ENSG00000221826	<i>PSG3</i>	7.39E-04	1.72E-03	-1.96
ENSG00000012779	<i>ALOX5</i>	1.14E-08	7.74E-07	-1.95
ENSG00000166825	<i>ANPEP</i>	2.67E-07	5.47E-06	-1.93
ENSG00000189052	<i>CGB5</i>	5.84E-05	2.53E-04	-1.93
ENSG00000168389	<i>MFSD2A</i>	3.37E-05	1.69E-04	-1.93
ENSG00000131620	<i>ANO1</i>	6.30E-05	2.69E-04	-1.93
ENSG00000156009	<i>MAGEA8</i>	2.72E-05	1.44E-04	-1.93
ENSG00000068831	<i>RASGRP2</i>	2.85E-08	1.36E-06	-1.92
ENSG00000196917	<i>HCAR1</i>	4.30E-08	1.73E-06	-1.92
ENSG00000110934	<i>BIN2</i>	1.01E-08	7.35E-07	-1.92
ENSG00000171124	<i>FUT3</i>	9.08E-08	2.74E-06	-1.92
ENSG00000104833	<i>TUBB4A</i>	2.85E-06	2.80E-05	-1.91
ENSG00000013297	<i>CLDN11</i>	1.69E-07	3.91E-06	-1.91
ENSG00000105472	<i>CLEC11A</i>	2.57E-08	1.29E-06	-1.91
ENSG00000070915	<i>SLC12A3</i>	7.44E-07	1.09E-05	-1.90
ENSG00000227932	<i>SELENOOLP</i>	7.28E-05	3.00E-04	-1.90
ENSG00000170848	<i>PSG6</i>	3.24E-05	1.64E-04	-1.89
ENSG00000100167	<i>SEPT3</i>	8.22E-09	6.68E-07	-1.89
ENSG00000214049	<i>UCA1</i>	5.80E-05	2.52E-04	-1.89
ENSG00000197172	<i>MAGEA6</i>	3.60E-03	5.87E-03	-1.88
ENSG00000204642	<i>HLA-F</i>	2.47E-07	5.18E-06	-1.88
ENSG00000206195	<i>DUXAP8</i>	1.58E-04	5.40E-04	-1.88
ENSG00000137948	<i>BRDT</i>	1.05E-02	1.35E-02	-1.87
ENSG00000213030	<i>CGB8</i>	1.13E-04	4.20E-04	-1.87
ENSG00000260266	<i>PPIAP46</i>	6.74E-05	2.83E-04	-1.86
ENSG00000080007	<i>DDX43</i>	4.38E-04	1.16E-03	-1.86
ENSG00000183688	<i>RFLNB</i>	1.67E-08	9.83E-07	-1.86
ENSG00000229142	<i>HCG4P8</i>	1.07E-09	1.98E-07	-1.86
ENSG00000165092	<i>ALDH1A1</i>	9.60E-05	3.70E-04	-1.85
ENSG00000251381	<i>LINC00958</i>	1.77E-03	3.36E-03	-1.84

ENSG00000171402	<i>XAGE3</i>	6.95E-04	1.64E-03	-1.83
ENSG00000104827	<i>CGB3</i>	1.82E-04	5.98E-04	-1.83
ENSG00000177464	<i>GPR4</i>	2.32E-08	1.22E-06	-1.83
ENSG00000184730	<i>APOBR</i>	9.53E-08	2.84E-06	-1.82
ENSG00000069122	<i>ADGRF5</i>	1.58E-07	3.79E-06	-1.81
ENSG00000127920	<i>GNG11</i>	1.52E-06	1.78E-05	-1.81
ENSG00000135318	<i>NT5E</i>	2.85E-04	8.46E-04	-1.81
ENSG00000143369	<i>ECM1</i>	2.25E-10	8.57E-08	-1.81
ENSG00000105641	<i>SLC5A5</i>	3.51E-04	9.86E-04	-1.80
ENSG00000133135	<i>RNF128</i>	3.28E-06	3.13E-05	-1.80
ENSG00000203783	<i>PRR9</i>	1.47E-03	2.92E-03	-1.80
ENSG00000145358	<i>DDIT4L</i>	1.82E-07	4.15E-06	-1.80
ENSG00000187268	<i>FAM9C</i>	2.24E-02	2.44E-02	-1.80
ENSG00000204832	<i>ST8SIA6-AS1</i>	1.69E-05	1.03E-04	-1.79
ENSG00000128340	<i>RAC2</i>	4.86E-09	5.05E-07	-1.79
ENSG00000182240	<i>BACE2</i>	4.03E-07	7.17E-06	-1.79
ENSG00000248810	<i>LINC02432</i>	3.45E-05	1.73E-04	-1.79
ENSG00000056291	<i>NPFFR2</i>	2.49E-07	5.22E-06	-1.78
ENSG00000104818	<i>CGB2</i>	2.28E-04	7.11E-04	-1.76
ENSG00000132517	<i>SLC52A1</i>	3.80E-06	3.45E-05	-1.75
ENSG00000137441	<i>FGFBP2</i>	6.17E-04	1.50E-03	-1.75
ENSG00000184029	<i>DSCR4</i>	2.33E-03	4.16E-03	-1.75
ENSG00000099399	<i>MAGEB2</i>	1.22E-03	2.52E-03	-1.75
ENSG00000196684	<i>HSH2D</i>	1.18E-05	7.92E-05	-1.74
ENSG00000266602	<i>AC008109.1</i>	1.73E-05	1.04E-04	-1.74
ENSG00000163492	<i>CCDC141</i>	2.21E-09	3.24E-07	-1.74
ENSG00000130829	<i>DUSP9</i>	2.34E-05	1.29E-04	-1.73
ENSG00000010310	<i>GIPR</i>	1.26E-08	8.38E-07	-1.73
ENSG00000107736	<i>CDH23</i>	1.50E-08	9.35E-07	-1.73
ENSG00000198054	<i>DSCR8</i>	3.66E-03	5.95E-03	-1.73
ENSG00000127585	<i>FBXL16</i>	1.06E-10	6.18E-08	-1.73
ENSG00000233828	<i>LINC01949</i>	1.26E-02	1.56E-02	-1.72
ENSG00000226088	<i>AL158839.1</i>	6.65E-09	6.17E-07	-1.72
ENSG00000268864	<i>AC011487.2</i>	1.30E-06	1.59E-05	-1.72
ENSG00000159713	<i>TPPP3</i>	3.63E-04	1.01E-03	-1.71
ENSG00000161681	<i>SHANK1</i>	2.13E-07	4.62E-06	-1.71
ENSG00000165272	<i>AQP3</i>	1.29E-06	1.58E-05	-1.71
ENSG00000105198	<i>LGALS13</i>	5.31E-04	1.34E-03	-1.71
ENSG00000012223	<i>LTF</i>	1.39E-03	2.79E-03	-1.70
ENSG00000105643	<i>ARRDC2</i>	2.73E-08	1.34E-06	-1.70
ENSG00000174156	<i>GSTA3</i>	1.10E-04	4.11E-04	-1.70
ENSG00000130475	<i>FCHO1</i>	5.59E-11	4.62E-08	-1.70
ENSG00000130876	<i>SLC7A10</i>	1.07E-04	4.04E-04	-1.70
ENSG00000165462	<i>PHOX2A</i>	2.69E-07	5.47E-06	-1.70
ENSG00000187621	<i>TCL6</i>	4.68E-04	1.22E-03	-1.69
ENSG00000009950	<i>MLXIPL</i>	2.89E-08	1.37E-06	-1.69
ENSG00000125895	<i>TMEM74B</i>	2.91E-08	1.37E-06	-1.69
ENSG00000280809	<i>LINC00836</i>	1.29E-03	2.63E-03	-1.69
ENSG00000091972	<i>CD200</i>	2.06E-04	6.58E-04	-1.69
ENSG00000248370	<i>LINC02434</i>	5.92E-04	1.45E-03	-1.68
ENSG00000124467	<i>PSG8</i>	2.25E-03	4.05E-03	-1.68
ENSG00000265190	<i>ANXA8</i>	3.19E-05	1.63E-04	-1.68
ENSG00000186847	<i>KRT14</i>	1.35E-03	2.73E-03	-1.68

ENSG00000105825	<i>TFPI2</i>	5.29E-06	4.39E-05	-1.68
ENSG00000156966	<i>B3GNT7</i>	1.20E-10	6.20E-08	-1.68
ENSG00000134533	<i>RERG</i>	3.28E-05	1.66E-04	-1.68
ENSG00000273297	<i>AC009275.1</i>	5.39E-07	8.61E-06	-1.68
ENSG00000164532	<i>TBX20</i>	4.54E-05	2.10E-04	-1.67
ENSG00000113249	<i>HAVCR1</i>	1.32E-04	4.71E-04	-1.67
ENSG00000242221	<i>PSG2</i>	2.06E-03	3.78E-03	-1.67
ENSG00000163898	<i>LIPH</i>	7.61E-07	1.11E-05	-1.67
ENSG00000183734	<i>ASCL2</i>	4.98E-07	8.17E-06	-1.67
ENSG00000107317	<i>PTGDS</i>	2.47E-06	2.53E-05	-1.67
ENSG00000161082	<i>CELF5</i>	1.28E-05	8.45E-05	-1.67
ENSG00000100558	<i>PLEK2</i>	9.82E-06	7.03E-05	-1.66
ENSG00000155657	<i>TTN</i>	4.66E-09	4.95E-07	-1.66
ENSG00000141255	<i>SPATA22</i>	1.19E-03	2.47E-03	-1.66
ENSG00000196878	<i>LAMB3</i>	2.10E-09	3.20E-07	-1.66
ENSG00000268756	<i>AC104534.1</i>	5.30E-08	1.98E-06	-1.66
ENSG00000046774	<i>MAGEC2</i>	1.07E-02	1.37E-02	-1.66
ENSG00000169164	<i>AL159987.1</i>	1.93E-03	3.60E-03	-1.65
ENSG00000123095	<i>BHLHE41</i>	6.09E-07	9.39E-06	-1.65
ENSG00000177679	<i>SRRM3</i>	1.55E-08	9.37E-07	-1.65
ENSG00000152804	<i>HHEX</i>	5.42E-05	2.40E-04	-1.65
ENSG00000176998	<i>HCG4</i>	4.25E-09	4.75E-07	-1.65
ENSG00000231208	<i>ZBTB46-AS1</i>	6.29E-04	1.52E-03	-1.65
ENSG00000269565	<i>GPR32P1</i>	3.35E-06	3.17E-05	-1.65
ENSG00000205795	<i>CYS1</i>	4.24E-06	3.76E-05	-1.64
ENSG00000163013	<i>FBXO41</i>	1.98E-12	4.16E-09	-1.64
ENSG00000103489	<i>XYLT1</i>	9.95E-08	2.93E-06	-1.64
ENSG00000241104	<i>CEACAMP10</i>	9.59E-03	1.26E-02	-1.63
ENSG00000271394	<i>RF00100</i>	6.74E-04	1.60E-03	-1.63
ENSG00000076864	<i>RAP1GAP</i>	3.59E-07	6.57E-06	-1.63
ENSG00000196337	<i>CGB7</i>	2.70E-04	8.10E-04	-1.63
ENSG00000129990	<i>SYT5</i>	4.93E-03	7.50E-03	-1.63
ENSG00000226080	<i>AC062028.2</i>	5.81E-06	4.74E-05	-1.63
ENSG00000173868	<i>PHOSPHO1</i>	1.50E-03	2.95E-03	-1.63
ENSG00000085563	<i>ABCB1</i>	1.20E-04	4.38E-04	-1.63
ENSG00000166961	<i>MS4A15</i>	4.17E-05	1.97E-04	-1.63
ENSG00000110436	<i>SLC1A2</i>	3.39E-04	9.59E-04	-1.63
ENSG00000130303	<i>BST2</i>	1.51E-03	2.97E-03	-1.63
ENSG00000124107	<i>SLPI</i>	3.86E-04	1.06E-03	-1.62
ENSG00000233215	<i>LINC01687</i>	9.44E-04	2.08E-03	-1.62
ENSG00000173890	<i>GPR160</i>	2.04E-11	2.38E-08	-1.62
ENSG00000157851	<i>DPYSL5</i>	5.96E-04	1.46E-03	-1.62
ENSG00000268601	<i>AC115522.1</i>	2.16E-06	2.30E-05	-1.62
ENSG00000267631	<i>CGB1</i>	3.00E-05	1.56E-04	-1.62
ENSG00000167680	<i>SEMA6B</i>	4.56E-07	7.76E-06	-1.62
ENSG00000092929	<i>UNC13D</i>	1.47E-08	9.22E-07	-1.62
ENSG00000166816	<i>LDHD</i>	1.32E-04	4.71E-04	-1.62
ENSG00000158825	<i>CDA</i>	3.07E-06	2.98E-05	-1.61
ENSG00000157766	<i>ACAN</i>	1.30E-02	1.60E-02	-1.61
ENSG00000272405	<i>AL365181.3</i>	2.09E-08	1.16E-06	-1.61
ENSG00000197182	<i>MIRLET7BHG</i>	6.39E-11	4.62E-08	-1.61
ENSG00000008735	<i>MAPK8IP2</i>	6.21E-09	5.98E-07	-1.61
ENSG00000147381	<i>MAGEA4</i>	1.17E-02	1.47E-02	-1.61

ENSG00000132677	<i>RHBG</i>	4.06E-10	1.04E-07	-1.61
ENSG00000183668	<i>PSG9</i>	1.68E-03	3.22E-03	-1.61
ENSG00000283023	<i>AC116618.1</i>	2.40E-03	4.26E-03	-1.61
ENSG00000179314	<i>WSCD1</i>	5.04E-06	4.22E-05	-1.61
ENSG00000104826	<i>LHB</i>	1.40E-04	4.91E-04	-1.61
ENSG00000141968	<i>VAV1</i>	4.37E-04	1.16E-03	-1.60
ENSG00000282870	<i>FRG1DP</i>	2.51E-03	4.40E-03	-1.60
ENSG00000166126	<i>AMN</i>	2.86E-10	9.35E-08	-1.60
ENSG00000140479	<i>PCSK6</i>	1.62E-09	2.66E-07	-1.60
ENSG00000183067	<i>IGSF5</i>	2.46E-04	7.51E-04	-1.60
ENSG00000223552	<i>AC098613.1</i>	1.29E-03	2.63E-03	-1.60
ENSG00000130821	<i>SLC6A8</i>	5.65E-09	5.62E-07	-1.60
ENSG00000204941	<i>PSG5</i>	5.28E-04	1.34E-03	-1.60
ENSG00000175274	<i>TP53I11</i>	5.87E-08	2.12E-06	-1.59
ENSG00000236417	<i>CTSLP1</i>	8.54E-07	1.20E-05	-1.59
ENSG00000238033	<i>AC002480.4</i>	1.67E-07	3.88E-06	-1.59
ENSG00000105696	<i>TMEM59L</i>	3.04E-05	1.57E-04	-1.59
ENSG00000065717	<i>TLE2</i>	3.57E-06	3.33E-05	-1.59
ENSG00000152527	<i>PLEKHH2</i>	2.44E-08	1.26E-06	-1.59
ENSG00000225210	<i>DUXAP9</i>	1.07E-03	2.29E-03	-1.59
ENSG00000268655	<i>AC008687.4</i>	4.28E-04	1.14E-03	-1.59
ENSG00000154764	<i>WNT7A</i>	4.12E-10	1.04E-07	-1.58
ENSG00000187569	<i>DPPA3</i>	3.31E-03	5.48E-03	-1.58
ENSG00000196639	<i>HRH1</i>	2.97E-08	1.39E-06	-1.58
ENSG00000065989	<i>PDE4A</i>	2.14E-08	1.17E-06	-1.58
ENSG00000228559	<i>AL033519.3</i>	7.24E-09	6.33E-07	-1.58
ENSG00000088836	<i>SLC4A11</i>	1.57E-08	9.40E-07	-1.58
ENSG00000105419	<i>MEIS3</i>	8.14E-07	1.15E-05	-1.58
ENSG00000126882	<i>FAM78A</i>	1.03E-04	3.92E-04	-1.58
ENSG00000142156	<i>COL6A1</i>	5.88E-07	9.15E-06	-1.58
ENSG00000266830	<i>AC061975.6</i>	1.44E-04	5.02E-04	-1.58
ENSG00000104722	<i>NEFM</i>	5.28E-04	1.34E-03	-1.58
ENSG00000163220	<i>SI00A9</i>	9.45E-05	3.66E-04	-1.58
ENSG00000141854	<i>MISP3</i>	5.51E-06	4.55E-05	-1.58
ENSG00000109610	<i>SOD3</i>	1.03E-06	1.34E-05	-1.58
ENSG00000214922	<i>HLA-F-AS1</i>	7.38E-10	1.52E-07	-1.58
ENSG00000163520	<i>FBLN2</i>	1.54E-08	9.37E-07	-1.58
ENSG00000138028	<i>CGREF1</i>	6.60E-07	9.98E-06	-1.58
ENSG00000248583	<i>AC119751.3</i>	1.81E-05	1.07E-04	-1.57
ENSG00000022267	<i>FHL1</i>	6.64E-07	1.00E-05	-1.57
ENSG00000231924	<i>PSG1</i>	7.59E-04	1.76E-03	-1.57
ENSG00000145063	<i>AC062028.1</i>	2.53E-05	1.37E-04	-1.57
ENSG00000152213	<i>ARL11</i>	1.13E-09	2.04E-07	-1.57
ENSG00000196209	<i>SIRPB2</i>	1.14E-04	4.23E-04	-1.57
ENSG00000168405	<i>CMAHP</i>	1.06E-06	1.37E-05	-1.57
ENSG00000225778	<i>PROSER2-AS1</i>	1.74E-02	2.01E-02	-1.57
ENSG00000149564	<i>ESAM</i>	6.14E-05	2.64E-04	-1.57
ENSG00000278704	<i>BX004987.1</i>	1.48E-03	2.92E-03	-1.57
ENSG00000173210	<i>ABLIM3</i>	2.18E-08	1.17E-06	-1.57
ENSG00000134326	<i>CMPK2</i>	1.63E-10	6.60E-08	-1.56
ENSG00000104059	<i>FAM189A1</i>	3.67E-04	1.02E-03	-1.56
ENSG00000177453	<i>NIM1K</i>	1.11E-08	7.69E-07	-1.56
ENSG00000006638	<i>TBXA2R</i>	4.68E-05	2.15E-04	-1.56

ENSG00000145623	<i>OSMR</i>	5.76E-05	2.51E-04	-1.56
ENSG00000101282	<i>RSPO4</i>	2.68E-03	4.65E-03	-1.56
ENSG00000168779	<i>SHOX2</i>	5.00E-06	4.20E-05	-1.56
ENSG00000102109	<i>PCSK1N</i>	1.18E-08	7.94E-07	-1.56
ENSG00000105639	<i>JAK3</i>	7.81E-11	4.88E-08	-1.56
ENSG00000231976	<i>FAM238B</i>	1.98E-05	1.14E-04	-1.56
ENSG00000079393	<i>DUSP13</i>	9.18E-06	6.71E-05	-1.56
ENSG00000229953	<i>AL590666.2</i>	2.22E-08	1.17E-06	-1.56
ENSG00000159871	<i>LYPD5</i>	8.02E-05	3.24E-04	-1.56
ENSG00000160179	<i>ABCG1</i>	3.45E-05	1.73E-04	-1.56
ENSG00000112195	<i>TREML2</i>	8.94E-03	1.20E-02	-1.56
ENSG00000261838	<i>AC092718.6</i>	1.11E-05	7.61E-05	-1.55
ENSG00000222612	<i>RNU2-52P</i>	5.27E-04	1.33E-03	-1.55
ENSG00000243137	<i>PSG4</i>	9.59E-04	2.11E-03	-1.55
ENSG00000133454	<i>MYO18B</i>	2.20E-02	2.41E-02	-1.55
ENSG00000111331	<i>OAS3</i>	2.90E-02	2.98E-02	-1.55
ENSG00000151702	<i>FLII</i>	3.94E-04	1.08E-03	-1.55
ENSG00000261371	<i>PECAM1</i>	7.45E-05	3.06E-04	-1.55
ENSG00000054598	<i>FOXC1</i>	3.61E-07	6.59E-06	-1.55
ENSG00000249125	<i>AC093821.1</i>	1.21E-03	2.50E-03	-1.55
ENSG00000124126	<i>PREX1</i>	1.73E-03	3.30E-03	-1.54
ENSG00000186897	<i>CIQL4</i>	2.95E-06	2.89E-05	-1.54
ENSG00000134716	<i>CYP2J2</i>	2.34E-03	4.18E-03	-1.54
ENSG00000188582	<i>PAQR9</i>	1.76E-04	5.84E-04	-1.54
ENSG00000169884	<i>WNT10B</i>	9.79E-06	7.02E-05	-1.54
ENSG00000282943	<i>AC004784.1</i>	2.82E-04	8.37E-04	-1.54
ENSG00000115194	<i>SLC30A3</i>	3.43E-04	9.69E-04	-1.54
ENSG00000077327	<i>SPAG6</i>	3.74E-06	3.42E-05	-1.54
ENSG00000267709	<i>AC024592.2</i>	5.29E-05	2.36E-04	-1.54
ENSG00000105376	<i>ICAM5</i>	1.07E-04	4.01E-04	-1.53
ENSG00000058091	<i>CDK14</i>	4.32E-06	3.82E-05	-1.53
ENSG00000074410	<i>CAI2</i>	4.68E-07	7.91E-06	-1.53
ENSG00000102891	<i>MT4</i>	1.07E-03	2.29E-03	-1.53
ENSG00000180438	<i>TPRXL</i>	2.70E-06	2.70E-05	-1.53
ENSG00000176387	<i>HSD11B2</i>	1.07E-03	2.29E-03	-1.53
ENSG00000100097	<i>LGALS1</i>	7.01E-09	6.30E-07	-1.53
ENSG00000273340	<i>MICE</i>	9.08E-09	6.89E-07	-1.53
ENSG00000255737	<i>AGAP2-AS1</i>	8.44E-10	1.70E-07	-1.53
ENSG00000142623	<i>PADI1</i>	1.33E-08	8.60E-07	-1.53
ENSG00000185112	<i>FAM43A</i>	1.09E-05	7.52E-05	-1.52
ENSG00000151025	<i>GPR158</i>	7.85E-05	3.18E-04	-1.52
ENSG00000157884	<i>CIB4</i>	2.52E-04	7.67E-04	-1.52
ENSG00000121552	<i>CSTA</i>	3.15E-06	3.04E-05	-1.52
ENSG00000114638	<i>UPK1B</i>	1.59E-05	9.89E-05	-1.52
ENSG00000198734	<i>F5</i>	9.29E-05	3.62E-04	-1.52
ENSG00000143119	<i>CD53</i>	1.47E-05	9.35E-05	-1.52
ENSG00000265060	<i>PPY2P</i>	2.08E-04	6.63E-04	-1.52
ENSG00000261761	<i>AL136537.2</i>	7.71E-03	1.07E-02	-1.52
ENSG00000189023	<i>MAGEB16</i>	4.28E-03	6.74E-03	-1.52
ENSG00000131746	<i>TNS4</i>	1.77E-05	1.06E-04	-1.52
ENSG00000172901	<i>LVRN</i>	4.02E-04	1.09E-03	-1.52
ENSG00000186564	<i>FOXD2</i>	2.98E-06	2.91E-05	-1.52
ENSG00000102452	<i>NALCN</i>	4.72E-06	4.05E-05	-1.52

ENSG00000203857	<i>HSD3B1</i>	3.56E-05	1.76E-04	-1.52
ENSG00000189221	<i>MAOA</i>	2.10E-05	1.19E-04	-1.52
ENSG00000123342	<i>MMP19</i>	2.95E-10	9.35E-08	-1.51
ENSG00000205413	<i>SAMD9</i>	7.41E-04	1.73E-03	-1.51
ENSG00000244306	<i>AL589743.1</i>	3.85E-04	1.06E-03	-1.51
ENSG00000168065	<i>SLC22A11</i>	4.94E-05	2.23E-04	-1.51
ENSG00000129993	<i>CBFA2T3</i>	2.25E-03	4.05E-03	-1.51
ENSG00000089847	<i>ANKRD24</i>	1.96E-08	1.13E-06	-1.51
ENSG00000214711	<i>CAPN14</i>	1.72E-05	1.04E-04	-1.51
ENSG00000020633	<i>RUNX3</i>	1.71E-05	1.04E-04	-1.51
ENSG00000130822	<i>PNCK</i>	1.11E-05	7.59E-05	-1.51
ENSG00000164647	<i>STEAP1</i>	5.68E-05	2.48E-04	-1.51
ENSG00000102362	<i>SYTL4</i>	1.22E-06	1.51E-05	-1.50
ENSG00000185168	<i>LINC00482</i>	3.04E-07	5.82E-06	-1.50
ENSG00000240694	<i>PNMA2</i>	1.64E-03	3.17E-03	-1.50
ENSG00000273143	<i>AL355512.1</i>	5.15E-08	1.95E-06	-1.50

Supplemental Table S9. Gene ontology (GO) categories identified as associated (p-value<0.01) with genes expressed at significantly higher expression levels in hPSC-TS^{CDX2} vs. hPSC-TS cells. Gene ontology categories are listed along with their respective p-values of enrichment, false discovery rate (FDR)-adjusted p-values of enrichment, and specific genes relevant to each gene ontology category.

Gene Ontology Category	p-value	FDR-adjusted p-value	Number of Genes with Significantly Higher Expression in hTESCs vs. hTSCs within GO Category	Genes with Significantly Higher Expression in hTESCs vs. hTSCs within GO Category
GO_REGULATION_OF_CELL_DIFFERENTIATION	1.24E-11	4.72E-08	64	ANKRD1, BOC, CDON, CDX2, CHN1, CNTN4, COL3A1, CRB2, CTNNA2, CXCL12, CXCL14, CXCR4, DLX2, DMTN, DPYSL3, FLRT2, GDF6, H2AFY2, HAS2, HEY2, HOXB8, ID4, IGFBP3, IRX3, ISL1, LEF1, LPAR1, LPL, MAF, MAFB, MAP1B, MAP2, MEF2C, NDNF, NR0B1, NREP, NTF3, PDPN, POSTN, PRKCQ, PROX1, RASGRP1, RELN, RGCC, RGS4, RUNX1T1, SDC2, SEMA3D, SLIT2, SMAD6, SMOC1, SORL1, SOSTDC1, SOX11, SOX5, SPPI, TCF4, TENM4, TFAP2B, TNRC6C, TRIB2, UST, WNT5B, ZEB2
GO_SKELETAL_SYSTEM_DEVELOPMENT	1.25E-11	4.72E-08	31	AUTS2, CDH11, CDX1, COL11A1, COL19A1, COL2A1, COL3A1, COL6A3, DLX2, DLX5, FREM1, GDF6, HAS2, HHIP, HMG2, HOXB5, HOXB6, HOXB8, HOXB9, HOXC4, HOXC8, LECT2, MAF, MATN2, MEF2C, PTH1R, SOX11, SOX5, SULF1, WFIKK1, WNT5B
GO_ANIMAL_ORGAN_MORPHOGENESIS	1.42E-11	4.72E-08	45	ACTA2, ANKRD1, AUTS2, CDON, CDX1, CDX2, COL11A1, COL2A1, COL3A1, COL6A3, CPE, CRB2, CTNNA2, DACT1, DLX2, DLX5, FLRT2, FREM1, GPC6, HAS2, HEY2, HHIP, HOXB5, HOXB6, HOXB8, HOXC4, HOXC8, ID4, IRX3, ISL1, KLHL3, LEF1, MAFB, MATN2, MEF2C, MYL3, NKD1, PROX1, SLIT2, SMAD6, SOSTDC1, SOX11, SULF1, TFAP2B, TNC
GO_EXTRACELLULAR_MATRIX	8.54E-11	2.13E-07	30	ADAMTS2, ADAMTS2L, ANGPTL2, CDH13, CDON, COL11A1, COL15A1, COL19A1, COL26A1, COL2A1, COL3A1, COL6A3, COL6A6, CXCL12, FLRT2, FREM1, GPC6, MATN2, MXRA5, NDNF, POSTN, RELN, SBSPON, SDC2, SERPINA5, SMOC1, SULF1, TNC, TRIL, WNT5B
GO_NEUROGENESIS	1.60E-10	3.21E-07	56	ANKRD1, APCDD1, AUTS2, BOC, CDH11, CDON, CHN1, CNTN4, COL3A1, CTNNA2, CXCL12, CXCR4, DLX2, DLX5, DPYSL3, FLRT2, GDF6, GRIN2A, HEY2, HHIP, HOXC8, ID4, IRX3, ISL1, LEF1, LPAR1, MAP1B, MAP2, MATN2, MEF2C, NDNF, NKD1, NREP, NTF3, POSTN, PRKCQ, PROX1, RELN, SDC2, SEMA3D, SH3GL2, SLIT2, SORL1, SOX11, SOX5, SPPI, TCF4, TENM2, TENM4, TNC, UNC5B, UNC5C, UST, WNT5B, ZEB2, ZNF521
GO_REGULATION_OF_CELL_DEVELOPMENT	4.24E-10	7.06E-07	40	ANKRD1, CDON, CHN1, CNTN4, COL3A1, CTNNA2, CXCL12, CXCR4, DLX2, DMTN, DPYSL3, FLRT2, GDF6, HAS2, HEY2, ID4, IRX3, ISL1, LPAR1, MAP1B, MAP2, MEF2C, NDNF, NREP, NTF3, PDPN, POSTN, PROX1, RELN, RGS4, SDC2, SEMA3D, SLIT2, SORL1, SOX11, SPPI, TCF4, TENM4, UST, ZEB2
GO_REGIONALIZATION	7.10E-10	9.17E-07	23	CDON, CDX1, CDX2, CRB2, DLX2, HEY2, HHIP, HOXB5, HOXB6, HOXB8, HOXB9, HOXC4, HOXC8, IRX3, ISL1, LEF1, MAFB, MEF2C, NKD1, RELN, SMAD6, SOSTDC1, ZEB2
GO_COLLAGEN_CONTAINING_EXTRACELLULAR_MATRIX	7.88E-10	9.17E-07	25	ADAMTS2, ANGPTL2, CDH13, CDON, COL11A1, COL15A1, COL19A1, COL26A1, COL2A1, COL3A1, COL6A3, COL6A6, CXCL12, FREM1, GPC6, MATN2, MXRA5, POSTN, SBSPON, SDC2, SERPINA5, SMOC1, SULF1, TNC, WNT5B
GO_NEURON_DIFFERENTIATION	8.26E-10	9.17E-07	49	ANKRD1, AUTS2, BOC, CDH11, CDON, CHN1, CNTN4, CTNNA2, CXCL12, CXCR4, DLX2, DLX5, DPYSL3, FLRT2, GDF6, HEY2, HOXC8, ID4, IRX3, ISL1, LPAR1, MAP1B, MAP2, MATN2, MEF2C, NDNF, NKD1, NREP, NTF3, POSTN, PRKCQ, PROX1, RELN, SDC2, SEMA3D, SH3GL2, SLIT2, SOX11, SPPI, TCF4, TENM2, TENM4, TNC, UNC5B, UNC5C, UST, WNT5B, ZEB2, ZNF521
GO_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	3.58E-09	3.58E-06	33	AUTS2, BOC, CDH11, CHN1, CNTN4, COL6A3, CTNNA2, CXCL12, CXCR4, DLX5, DMTN, FLRT2, HAS2, HRH2, ISL1, LEF1, MAP1B, MAP2, MATN2, MEF2C, PDPN, POSTN, PRKCQ, PROX1, RELN, SDC2, SEMA3D, SLIT2, SPPI, UNC5B, UNC5C, UST, ZEB2
GO_CELLULAR_COMPONENT_MORPHOGENESIS	5.81E-09	5.28E-06	42	ANKRD1, AUTS2, BOC, CDH11, CDH13, CDH7, CHN1, CNTN4, COL6A3, CTNNA2, CXCL12, CXCR4, DLX5, DMTN, FGD5, FLRT2, HAS2, HRH2, ISL1, LEF1, LPAR1, MAP1B, MAP2, MATN2, MEF2C, NTF3, PDPN, PLA2G3, POSTN, PRKCQ, PROX1, RELN, SDC2, SEMA3D, SH3GL2, SLIT2, SPPI, TENM4, UNC5B, UNC5C, UST, ZEB2
GO_SKELETAL_SYSTEM_MORPHOGENESIS	8.73E-09	7.27E-06	18	AUTS2, CDX1, COL11A1, COL2A1, COL6A3, DLX2, DLX5, FREM1, HAS2, HHIP, HOXB5, HOXB6, HOXB8, HOXC4, HOXC8, MATN2, MEF2C, SOX11
GO_REGULATION_OF_NEURON_DIFFERENTIATION	1.34E-08	1.03E-05	30	ANKRD1, CDON, CHN1, CNTN4, CTNNA2, CXCL12, DLX2, DPYSL3, GDF6, HEY2, ID4, IRX3, ISL1, LPAR1, MAP1B, MAP2, MEF2C, NDNF, NREP, NTF3, PROX1, RELN, SDC2, SEMA3D, SLIT2, SOX11, SPPI, TCF4, UST, ZEB2
GO_TISSUE_MORPHOGENESIS	1.96E-08	1.40E-05	30	ACTA2, ANKRD1, COL11A1, COL3A1, COL6A3, CRB2, DACT1, EDNRA, EYA2, GPC6, HEY2, HHIP, HMG2, ID4, IRX3, ISL1, KLHL3, LEF1, MATN2, MEF2C, MYL3, NKD1, PDPN, PROX1, SLIT2, SOSTDC1, SOX11, SULF1, TNC, ZEB2
GO_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	2.66E-08	1.77E-05	36	ANKRD1, CDON, CHN1, CNTN4, COL3A1, CTNNA2, CXCL12, CXCR4, DLX2, DPYSL3, FLRT2, GDF6, HEY2, ID4, IRX3, ISL1, LPAR1, LRFN5, MAP1B, MAP2, MEF2C, NDNF, NREP, NTF3, PROX1, RELN, SDC2, SEMA3D, SLIT2, SORL1, SOX11, SPPI, TCF4, TENM4, UST, ZEB2
GO_PATTERN_SPECIFICATION_PROCESS	6.84E-08	4.07E-05	23	CDON, CDX1, CDX2, CRB2, DLX2, HEY2, HHIP, HOXB5, HOXB6, HOXB8, HOXB9, HOXC4, HOXC8, IRX3, ISL1, LEF1, MAFB, MEF2C, NKD1, RELN, SMAD6, SOSTDC1, ZEB2
GO_AXON_DEVELOPMENT	6.91E-08	4.07E-05	25	AUTS2, BOC, CDH11, CHN1, CNTN4, CTNNA2, CXCL12, CXCR4, DLX5, FLRT2, ISL1, MAP1B, MAP2, MATN2, NREP, PRKCQ, RELN, SEMA3D, SLIT2, SPPI, TNC, UNC5B, UNC5C, UST, ZEB2

GO_BIOLOGICAL_ADHESION	9.26E-08	5.14E-05	46	ADAMTS18, BOC, CADM3, CDH11, CDH13, CDH7, CDON, CNTN4, COL15A1, COL19A1, COL26A1, COL3A1, COL6A3, COL6A6, CRB2, CTNNA2, CXCL12, CXCR4, CYP1B1, DMTN, FLRT2, FREM1, HAS2, HLA-DPB1, KIRREL1, LEF1, LRFN5, LRRRC4, LSAMP, NDNF, PCDH18, PCDH7, PCDHB15, PCDHB5, PDE3B, PDPN, POSTN, PRKCQ, RASGRP1, RELN, RGCC, SMAD6, SPPI, TENM2, TENM4, TNC
GO_CHONDROCYTE_DIFFERENTIATION	1.24E-07	6.53E-05	12	COL11A1, COL2A1, COL6A3, GDF6, HMG2, MAF, MATN2, MEFC2, PTH1R, SOX5, SULF1, WNT5B
GO_POSITIVE_REGULATION_OF_CELL_DIFFERENTIATION	1.71E-07	8.53E-05	36	ANKRD1, BOC, CDON, CDX2, CRB2, CTNNA2, CXCL12, CXCR4, DLX2, DMTN, DPYSL3, GDF6, H2AFY2, HAS2, ID4, IGFBP3, IRX3, ISL1, LEF1, LPAR1, LPL, MAP1B, MEFC2C, NDNF, PDPN, PROX1, RASGRP1, RELN, RGCC, SLIT2, SOX11, SOX5, TCF4, TENM4, WNT5B, ZEB2
GO_EMBRYONIC_SKELETAL_SYSTEM_DEVELOPMENT	2.33E-07	1.11E-04	12	AUTS2, COL11A1, COL2A1, DLX2, HOXB5, HOXB6, HOXB8, HOXB9, HOXC4, MEFC2C, SOX11, SULF1
GO_CELL_PART_MORPHOGENESIS	3.80E-07	1.73E-04	28	AUTS2, BOC, CDH11, CHN1, CNTN4, CTNNA2, CXCL12, CXCR4, DLX5, FLRT2, ISL1, MAP1B, MAP2, MATN2, NTF3, PDPN, POSTN, PRKCQ, RELN, SDC2, SEMA3D, SH3GL2, SLIT2, SPPI, UNC5B, UNC5C, UST, ZEB2
GO_CELL_MORPHOGENESIS_INVOLVED_IN_NEURON_DIFFERENTIATION	7.29E-07	3.17E-04	25	AUTS2, BOC, CDH11, CHN1, CNTN4, CTNNA2, CXCL12, CXCR4, DLX5, FLRT2, ISL1, MAP1B, MAP2, MATN2, MEFC2C, PRKCQ, RELN, SDC2, SEMA3D, SLIT2, SPPI, UNC5B, UNC5C, UST, ZEB2
GO_EMBRYONIC_SKELETAL_SYSTEM_MORPHOGENESIS	8.62E-07	3.59E-04	10	AUTS2, COL11A1, COL2A1, DLX2, HOXB5, HOXB6, HOXB8, HOXC4, MEFC2C, SOX11
GO_LOCOMOTION	9.14E-07	3.65E-04	54	APCDD1, AUTS2, BOC, C5, CDH13, CHN1, CNTN4, COL3A1, CRB2, CTNNA2, CXCL12, CXCL14, CXCR4, CYP1B1, DACH1, DLX5, DMTN, DPYSL3, FAM110C, FLRT2, GPC6, GRIN2A, GYPC, HAS2, HOXB9, IGFBP3, ISL1, LECT2, LEF1, LPAR1, MAP1B, MATN2, MEFC2C, NDNF, NKD1, NTF3, OPRK1, PDPN, PHACTR1, PLA2G3, POSTN, PRKCQ, PROX1, RELN, RGCC, SDC2, SEMA3D, SLIT2, SORL1, SULF1, UNC5B, UNC5C, WNT5B, ZEB2
GO_CONNECTIVE_TISSUE_DEVELOPMENT	1.53E-06	5.57E-04	16	ACTA2, COL11A1, COL2A1, COL6A3, DLX2, GDF6, HMG2, HOXC4, ID4, MAF, MATN2, MEFC2C, PTH1R, SOX5, SULF1, WNT5B
GO_CARTILAGE_DEVELOPMENT	1.56E-06	5.57E-04	14	COL11A1, COL2A1, COL6A3, DLX2, GDF6, HMG2, HOXC4, MAF, MATN2, MEFC2C, PTH1R, SOX5, SULF1, WNT5B
GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT_CONFERRING_TENSILE_STRENGTH	1.56E-06	5.57E-04	7	COL11A1, COL15A1, COL19A1, COL2A1, COL3A1, COL6A3, COL6A6
GO_ANTERIOR_POSTERIOR_PATTERN_SPECIFICATION	1.96E-06	6.74E-04	14	CDON, CDX1, CDX2, CRB2, HEY2, HOXB5, HOXB6, HOXB8, HOXB9, HOXC4, HOXC8, LEF1, NKD1, ZEB2
GO_NEURON_DEVELOPMENT	2.13E-06	7.10E-04	36	ANKRD1, AUTS2, BOC, CDH11, CHN1, CNTN4, CTNNA2, CXCL12, CXCR4, DLX5, DPYSL3, FLRT2, ISL1, LPAR1, MAP1B, MAP2, MATN2, MEFC2C, NDNF, NRPE, NTF3, POSTN, PRKCQ, RELN, SDC2, SEMA3D, SH3GL2, SLIT2, SPPI, TENM2, TENM4, TNC, UNC5B, UNC5C, UST, ZEB2
GO_EMBRYONIC_MORPHOGENESIS	2.65E-06	8.55E-04	24	AFF3, AUTS2, CDON, COL11A1, COL2A1, CRB2, DACT1, DLX2, DLX5, EYA2, HMG2, HOXB5, HOXB6, HOXB8, HOXC4, IRX3, LEF1, MAFB, MEFC2C, PROX1, SOX11, SULF1, TENM4, ZEB2
GO_EXTRACELLULAR_MATRIX_STRUCTURAL_CONSTITUENT	3.43E-06	1.07E-03	12	COL11A1, COL15A1, COL19A1, COL2A1, COL3A1, COL6A3, COL6A6, MATN2, MXR45, POSTN, SBSPO, TNC
GO_EMBRYO_DEVELOPMENT	4.24E-06	1.28E-03	33	AFF3, AUTS2, C5, CDON, CDX1, CDX2, COL11A1, COL2A1, CRB2, DACT1, DLX2, DLX5, EDNRA, EYA2, HEY2, HMG2, HOXB5, HOXB6, HOXB8, HOXB9, HOXC4, IRX3, ISL1, LEF1, MAFB, MEFC2C, NKD1, PROX1, SMAD6, SOX11, SULF1, TENM4, ZEB2
GO_NEGATIVE_REGULATION_OF_CELL_DEVELOPMENT	6.18E-06	1.82E-03	17	CNTN4, COL3A1, DLX2, DMTN, DPYSL3, ID4, IRX3, ISL1, LPAR1, MAP2, POSTN, RGS4, SEMA3D, SLIT2, SORL1, SOX11, SPPI
GO_TUBE_DEVELOPMENT	6.65E-06	1.90E-03	35	ADAMTS2, ADAMTS2L, C5, CDH13, CDX2, COL15A1, COL2A1, COL3A1, CYP1B1, DACT1, EDNRA, HAS2, HEY2, HHIP, HMG2, HRH2, IRX3, ISL1, KLHL3, LEF1, MEFC2C, NDNF, PDE3B, PDPN, PROX1, RGCC, SLIT2, SMAD6, SOSTDC1, SOX11, SULF1, TFAP2B, TNC, UNC5B, ZEB2
GO_NEURON_PROJECTION_GUIDANCE	7.83E-06	2.13E-03	15	BOC, CHN1, CNTN4, CXCL12, CXCR4, DLX5, FLRT2, ISL1, MATN2, PRKCQ, RELN, SEMA3D, SLIT2, UNC5B, UNC5C
GO_CARDIAC_VENTRICLE_MORPHOGENESIS	7.89E-06	2.13E-03	8	COL11A1, CPE, HEY2, ISL1, MEFC2C, MYL3, PROX1, SOX11
GO_POSITIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	8.83E-06	2.27E-03	41	ANKRD1, BOC, C5, CDON, CDX2, CRB2, CTNNA2, CXCL12, CXCR4, CYP1B1, DLX2, DMTN, DPYSL3, FLRT2, GDF6, H2AFY2, HAS2, HEY2, HMG2, ID4, IGFBP3, IRX3, ISL1, LEF1, LPAR1, LPL, MAP1B, MEFC2C, NDNF, PDPN, PROX1, RASGRP1, RELN, RGCC, SLIT2, SOX11, SOX5, TCF4, TENM4, WNT5B, ZEB2
GO_CENTRAL_NERVOUS_SYSTEM_DEVELOPMENT	9.32E-06	2.27E-03	32	AUTS2, CDH11, CDON, CNTN4, COL2A1, COL3A1, CTNNA2, CXCL12, CXCR4, DLX2, DLX5, GRIN2A, H2AFY2, HOXB8, ID4, ISL1, KIF1A, LEF1, LPAR1, MAFB, MAP2, NR0B1, PCDH18, PROX1, RELN, RGS4, SH3GL2, SLIT2, SOX11, TENM4, UNC5C, ZEB2
GO_EMBRYO_DEVELOPMENT_ENDING_IN_BIRTH_OR_EGG_HATCHING	9.41E-06	2.27E-03	24	AUTS2, C5, CDX1, CDX2, COL11A1, COL2A1, CRB2, DACT1, DLX2, EDNRA, HEY2, HOXB5, HOXB6, HOXB8, HOXB9, HOXC4, ISL1, LEF1, MEFC2C, NKD1, PROX1, SOX11, SULF1, ZEB2
GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION	9.48E-06	2.27E-03	19	ADAMTS2, ADAMTS2L, COL11A1, COL15A1, COL19A1, COL2A1, COL3A1, COL6A3, CYP1B1, FLRT2, HAS2, LPL, NDNF, PDPN, POSTN, RGCC, SPPI, SULF1, TNC
GO_ANATOMICAL_STRUCTURE_FORMATION_INVOLVED_IN_MORPHOGENESIS	9.54E-06	2.27E-03	36	ANKRD1, C5, CDH13, CDON, CDX1, CDX2, COL11A1, COL15A1, COL2A1, CRB2, CYP1B1, DLX5, EDNRA, EYA2, HEY2, HMG2, IRX3, ISL1, LEF1, MAFB, MEFC2C, NDNF, NKD1, PDE3B, PDPN, PLA2G3, PROX1, RELN, RGCC, SLIT2, SOX11, SULF1, TENM4, TFAP2B, UNC5B, ZEB2
GO_CARDIAC_VENTRICLE_DEVELOPMENT	1.24E-05	2.87E-03	10	COL11A1, CPE, HEY2, ISL1, MEFC2C, MYL3, PROX1, SLIT2, SMAD6, SOX11

GO_MESENCHYMAL_CELL_DIFFERENTIATION	1.38E-05	3.13E-03	13	CRB2, EDNRA, HAS2, HEY2, HMG2, ISL1, LEF1, MEF2C, PDPN, RGCC, SEMA3D, SOX11, ZEB2
GO_HEAD_DEVELOPMENT	1.44E-05	3.20E-03	27	AUTS2, CDON, CNTN4, COL2A1, COL3A1, CTNNA2, CXCL12, CXCR4, DLX2, DLX5, EDNRA, GRIN2A, H2AFY2, ID4, ISL1, KIF1A, LEF1, LPAR1, MAFB, NR0B1, PCDH18, PROX1, RELN, RGS4, SLIT2, UNC5C, ZEB2
GO_CARDIAC_CHAMBER_MORPHOGENESIS	1.52E-05	3.30E-03	10	COL11A1, CPE, HEY2, ISL1, MEF2C, MYL3, PROX1, SLIT2, SMAD6, SOX11
GO_RESPONSE_TO_GROWTH_FACTOR	1.64E-05	3.49E-03	26	ADAMTS12, ANKRD1, COL2A1, COL3A1, CRB2, DLX5, FLRT2, GDF6, HAS2, HHIP, LEF1, MEF2C, MXRA5, NREP, NTF3, POSTN, SH3GL2, SLIT2, SMAD6, SOSTDC1, SOX11, SOX5, SULF1, TFAP2B, TNC, WFIKKN1
GO_HEART_MORPHOGENESIS	1.72E-05	3.59E-03	14	ANKRD1, COL11A1, COL2A1, CPE, FLRT2, HAS2, HEY2, ISL1, MEF2C, MYL3, PROX1, SLIT2, SMAD6, SOX11
GO_CELL_MOTILITY	1.82E-05	3.60E-03	46	APCDD1, AUTS2, C5, CDH13, COL3A1, CRB2, CTNNA2, CXCL12, CXCL14, CXCR4, CYP1B1, DACHI, DMTN, DPYSL3, FAM110C, FLRT2, GPC6, GYPC, HAS2, HOXB9, IGFBP3, ISL1, LEF1, LPAR1, MAP1B, MATN2, MEF2C, NDNF, NKD1, NTF3, PDPN, PHACTR1, PLA2G3, POSTN, PRKCQ, PROX1, RELN, RGCC, SDC2, SEMA3D, SLIT2, SORL1, SULF1, UNC5C, WNT5B, ZEB2
GO_CELL_CELL_ADHESION	1.83E-05	3.60E-03	28	ADAMTS18, CADM3, CDH11, CDH13, CDH7, CNTN4, COL19A1, CRB2, CTNNA2, CXCL12, CYP1B1, DMTN, HAS2, HLA-DPB1, KIRREL1, LEF1, LRFN5, LRRC4, PCDH18, PCDH7, PCDHB15, PCDHB5, PDPN, PRKCQ, RASGRP1, RGCC, TENM2, TENM4
GO_CELL_PROJECTION_ORGANIZATION	1.87E-05	3.60E-03	42	ANKRD1, AUTS2, BOC, CDH11, CDH13, CHN1, CNTN4, CTNNA2, CXCL12, CXCR4, DLX5, DMTN, DPYSL3, EMP1, FAM110C, FGD5, FLRT2, ISL1, LPAR1, MAP1B, MAP2, MATN2, MEF2C, NDNF, NREP, NTF3, PDPN, PLA2G3, POSTN, PRKCQ, RELN, SDC2, SEMA3D, SH3GL2, SLIT2, SPP1, TENM2, TNC, UNC5B, UNC5C, UST, ZEB2
GO_POSITIVE_REGULATION_OF_NEURON_DIFFERENTIATION	1.88E-05	3.60E-03	17	ANKRD1, CDON, CXCL12, DLX2, DPYSL3, GDF6, IRX3, LPAR1, MAP1B, MEF2C, NDNF, PROX1, RELN, SLIT2, SOX11, TCF4, ZEB2
GO_CIRCULATORY_SYSTEM_DEVELOPMENT	1.91E-05	3.60E-03	35	ACTA2, ANKRD1, C5, CDH13, CDX2, COL11A1, COL15A1, COL2A1, COL3A1, CPE, CRB2, CYP1B1, EDNRA, FLRT2, HAS2, HEY2, HMG2, ISL1, KCNJ8, LEF1, MEF2C, MYL3, NDNF, PDE3B, PDPN, PROX1, RGCC, RGS4, SLIT2, SMAD6, SOX11, SULF1, TENM4, TFAP2B, UNC5B
GO_ENHANCER_BINDING	1.98E-05	3.67E-03	10	CDX1, CDX2, HOXB5, HOXB6, HOXC4, ISL1, LEF1, MEF2C, SOX11, TFAP2B
GO_NEGATIVE_REGULATION_OF_CELL_DIFFERENTIATION	2.02E-05	3.68E-03	26	CNTN4, COL3A1, CXCL14, DLX2, DMTN, DPYSL3, HEY2, HOXB8, ID4, IRX3, ISL1, LPAR1, MAFB, MAP2, NR0B1, POSTN, RGS4, RUNX1T1, SEMA3D, SLIT2, SMAD6, SORL1, SOSTDC1, SOX11, SPPI, TRIB2
GO_SYNAPSE	2.28E-05	4.05E-03	35	CADM3, CDH11, CDH13, CNKSR2, CPE, CTNNA2, DACT1, DLGAP1, DMTN, DPYSL3, FLRT2, GABRP, GPC6, GRIN2A, GUCY1A1, KCNMA1, KIF1A, LPAR1, LRFN5, LRRC4, MAP1B, MAP2, MEF2C, NTF3, OPRK1, PDZRN3, PHACTR1, POSTN, SH3GL2, SHISA6, SHISA9, SNTB1, SYT10, TENM2, UNC5C
GO_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	2.31E-05	4.05E-03	15	CHN1, CXCL12, DMTN, HAS2, MAP1B, MAP2, PDPN, POSTN, RELN, SDC2, SEMA3D, SLIT2, SPP1, UST, ZEB2
GO_EPITHELIUM_DEVELOPMENT	2.60E-05	4.48E-03	37	ACTA2, ADAMTS12, AKRIC2, APCDD1, CDX1, CDX2, CES1, COL2A1, CRB2, DACT1, DLX5, EDNRA, GPC6, H2AFY2, HEY2, HHIP, HOXB5, HRH2, ID4, IRX3, KLHL3, LEF1, MAF, MEF2C, NKD1, NR0B1, PDPN, PROX1, SLIT2, SMAD6, SOSTDC1, SOX11, SULF1, TFAP2B, TNC, WNT5B, ZEB2
GO_NEGATIVE_REGULATION_OF_DEVELOPMENTAL_PROCESS	2.75E-05	4.66E-03	32	CNTN4, COL3A1, CXCL14, DLX2, DMTN, DPYSL3, HEY2, HMG2, HOXB8, ID4, IRX3, ISL1, LEF1, LPAR1, MAFB, MAP2, NKD1, NR0B1, PDE3B, POSTN, RGCC, RGS4, RUNX1T1, SEMA3D, SLIT2, SMAD6, SORL1, SOSTDC1, SOX11, SPPI, SULF1, TRIB2
GO_COLLAGEN_TRIMER	3.21E-05	5.35E-03	8	COL11A1, COL15A1, COL19A1, COL26A1, COL2A1, COL3A1, COL6A3, COL6A6
GO_ENDOPLASMIC_RETICULUM_LUMEN	3.39E-05	5.55E-03	15	ARSI, CES1, COL11A1, COL15A1, COL19A1, COL26A1, COL2A1, COL3A1, COL6A3, IGFBP3, NOTUM, SDC2, SPPI, TNC, WNT5B
GO_POSITIVE_REGULATION_OF_CELL_DEVELOPMENT	3.45E-05	5.56E-03	21	ANKRD1, CDON, CXCL12, CXCR4, DLX2, DMTN, DPYSL3, GDF6, HAS2, IRX3, LPAR1, MAP1B, MEF2C, NDNF, PROX1, RELN, SLIT2, SOX11, TCF4, TENM4, ZEB2
GO_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	3.81E-05	6.05E-03	14	CADM3, CDH11, CDH13, CDH7, CNTN4, CRB2, LRFN5, LRRC4, PCDH18, PCDH7, PCDHB15, PCDHB5, TENM2, TENM4
GO_TAXIS	3.90E-05	6.09E-03	23	BOC, C5, CDH13, CHN1, CNTN4, CXCL12, CXCL14, CXCR4, DLX5, FLRT2, HOXB9, ISL1, LECT2, LEF1, LPAR1, MATN2, NTF3, PRKCQ, RELN, SEMA3D, SLIT2, UNC5B, UNC5C
GO_REGULATION_OF_ANATOMICAL_STRUCTURE_MORPHOGENESIS	3.96E-05	6.09E-03	34	C5, CDX1, CDX2, CHN1, CRB2, CXCL12, CYP1B1, DACT1, DMTN, FGD5, GPC6, HAS2, HEY2, HMG2, ISL1, LPAR1, MAP1B, MAP2, MEF2C, NKD1, PDE3B, PDPN, POSTN, PROX1, RELN, RGCC, SDC2, SEMA3D, SLIT2, SPPI, SULF1, TENM4, UST, ZEB2
GO_MESENCHYME_DEVELOPMENT	4.13E-05	6.25E-03	14	ACTA2, CRB2, EDNRA, HAS2, HEY2, HMG2, ISL1, LEF1, MEF2C, PDPN, RGCC, SEMA3D, SOX11, ZEB2
GO_EMBRYONIC_ORGAN_MORPHOGENESIS	5.62E-05	8.39E-03	14	AUTS2, COL11A1, COL2A1, CRB2, DLX2, DLX5, HOXB5, HOXB6, HOXB8, HOXC4, MAFB, MEF2C, PROX1, SOX11
GO_NEURON_MIGRATION	6.96E-05	1.02E-02	10	AUTS2, COL3A1, CTNNA2, CXCL12, FLRT2, MAP1B, MATN2, MEF2C, NDNF, RELN
GO_POSITIVE_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	7.84E-05	1.14E-02	20	ANKRD1, CDON, CXCL12, CXCR4, DLX2, DPYSL3, FLRT2, GDF6, IRX3, LPAR1, MAP1B, MEF2C, NDNF, PROX1, RELN, SLIT2, SOX11, TCF4, TENM4, ZEB2
GO_REGULATION_OF_PLATELET_AGGREGATION	8.05E-05	1.15E-02	4	ADAMTS18, DMTN, PDPN, PRKCQ
GO_CELL_FATE_COMMITMENT	8.97E-05	1.26E-02	13	CDON, DLX2, EYA2, HEY2, ISL1, MEF2C, PDPN, PROX1, SOSTDC1, SOX5, TENM4, WNT5B, ZNF521
GO_BASAL_DENDRITE	9.39E-05	1.29E-02	3	MAP1B, MAP2, SH3GL2

GO_CORTICOSPINAL_TRACT_MORPHOGENESIS	9.39E-05	1.29E-02	3	CDH11, SLIT2, ZEB2
GO_NEGATIVE_REGULATION_OF_DNA_BINDING	9.95E-05	1.33E-02	6	HEY2, HMG42, ID4, LEF1, SOX11, WFIKKN1
GO_REGULATION_OF_MYOBlast_DIFFERENTIATION	9.95E-05	1.33E-02	6	BOC, CDON, CXCL14, IGFBP3, MEF2C, SOSTDC1
GO_SEGMENTATION	1.08E-04	1.40E-02	8	CDX1, CDX2, CRB2, IRX3, LEF1, MAFB, NKD1, ZEB2
GO_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	1.08E-04	1.40E-02	45	AIM2, ANKRD1, C5, CDON, CRB2, CXCL12, CXCR4, CYP1B1, DLX2, DMTN, DPYSL3, FLRT2, GDF6, H2AFY2, HAS2, HEY2, HLA-DPB1, HMG42, HRH2, ID4, IRX3, ISL1, LEF1, LPAR1, LPL, MAPIB, MEF2C, NDNF, PDE9A, PDPN, POSTN, PRKCQ, PROX1, RASGRP1, RELN, RGCC, RGS4, SLIT2, SOX11, SOX5, SPPI, SULF1, TCF4, TENM4, ZEB2
GO_TUBE_MORPHOGENESIS	1.09E-04	1.40E-02	28	C5, CDH13, COL15A1, COL3A1, CYP1B1, DACT1, EDNRA, HAS2, HEY2, HHIP, HMG42, IRX3, ISL1, KLHL3, LEF1, MEF2C, NDNF, PDE3B, PROX1, RGCC, SLIT2, SOSTDC1, SOX11, SULF1, TFAP2B, TNC, UNC5B, ZEB2
GO_DEVELOPMENTAL_GROWTH_INVOLVED_IN_MORPHOGENESIS	1.12E-04	1.41E-02	12	AUTS2, CXCL12, MAPIB, MAP2, NKD1, POSTN, SEMA3D, SH3GL2, SLIT2, SPPI, TNC, ZEB2
GO_FOREBRAIN_DEVELOPMENT	1.13E-04	1.41E-02	16	AUTS2, CDON, COL3A1, CXCL12, DLX2, DLX5, ID4, ISL1, KIF1A, LEF1, LPAR1, NR0B1, PROX1, RELN, SLIT2, ZEB2
GO_EMBRYONIC_ORGAN_DEVELOPMENT	1.17E-04	1.43E-02	17	AUTS2, CDX2, COL11A1, COL2A1, CRB2, DLX2, DLX5, HEY2, HOXB5, HOXB6, HOXB8, HOXC4, LEF1, MAFB, MEF2C, PROX1, SOX11
GO_NEGATIVE_REGULATION_OF_BINDING	1.18E-04	1.43E-02	10	DACT1, HEY2, HMG42, ID4, ISL1, LEF1, MAP2, SORL1, SOX11, WFIKKN1
GO_NEGATIVE_REGULATION_OF_NERVOUS_SYSTEM_DEVELOPMENT	1.24E-04	1.50E-02	14	CNTN4, COL3A1, DLX2, DPYSL3, ID4, IRX3, ISL1, LPAR1, MAP2, SEMA3D, SLIT2, SORL1, SOX11, SPPI
GO_CARDIAC_CHAMBER_DEVELOPMENT	1.37E-04	1.60E-02	10	COL11A1, CPE, HEY2, ISL1, MEF2C, MYL3, PROX1, SLIT2, SMAD6, SOX11
GO_RESPONSE_TO_BMP	1.37E-04	1.60E-02	10	COL2A1, CRB2, DLX5, GDF6, LEF1, SMAD6, SOSTDC1, SOX11, SULF1, TFAP2B
GO_REGULATION_OF_CELLULAR_COMPONENT_MOVEMENT	1.38E-04	1.60E-02	31	C5, CDH13, COL3A1, CTNNA2, CXCL12, CXCL14, CYP1B1, DACT1, DMTN, DPYSL3, FAM110C, FLRT2, HAS2, IGFBP3, LEF1, LPAR1, MAP2, MEF2C, NKD1, NTF3, PDPN, POSTN, PROX1, RELN, RGCC, SEMA3D, SLIT2, SORL1, SULF1, UNC5C, WNT5B
GO_PROTEOGLYCAN_BINDING	1.44E-04	1.65E-02	5	ADA2, COL2A1, LPL, SLIT2, TNC
GO_POSITIVE_REGULATION_OF_CELL_PROLIFERATION_IN_BONE_MARROW	1.49E-04	1.69E-02	3	HMG42, LEF1, MEF2C
GO_MYOBlast_DIFFERENTIATION	1.87E-04	2.10E-02	7	BOC, CDON, CXCL14, IGFBP3, ISL1, MEF2C, SOSTDC1
GO_BONE_MORPHOGENESIS	1.93E-04	2.14E-02	8	CDX1, COL2A1, COL6A3, DLX5, FREM1, HAS2, MATN2, MEF2C
GO_CARDIOVASCULAR_SYSTEM_DEVELOPMENT	2.07E-04	2.27E-02	25	ACTA2, C5, CDH13, CDX2, COL15A1, COL3A1, CRB2, CYP1B1, EDNRA, HAS2, HEY2, HMG42, ISL1, LEF1, MEF2C, NDNF, PDE3B, PDPN, PROX1, RGCC, SLIT2, SMAD6, SULF1, TFAP2B, UNC5B
GO_REGULATION_OF_CELL_PROJECTION_ORGANIZATION	2.16E-04	2.34E-02	22	ANKRD1, AUTS2, CHN1, CTNNA2, CXCL12, DMTN, DPYSL3, FAM110C, LPAR1, MAPIB, MAP2, MEF2C, NDNF, PDPN, RELN, SDC2, SEMA3D, SLIT2, SPPI, TENM2, UST, ZEB2
GO_REGULATION_OF_SOMITOGENESIS	2.21E-04	2.37E-02	3	CDX1, CDX2, NKD1
GO_SENSORY_ORGAN_DEVELOPMENT	2.34E-04	2.46E-02	19	ADAMTS18, CDON, COL11A1, COL2A1, CXCL14, CYP1B1, DLX2, DLX5, HEY2, LEF1, MAF, MAFB, NKD1, PROX1, SMOC1, SOX11, TFAP2B, WNT5B, ZEB2
GO_POSITIVE_REGULATION_OF_MYOBlast_DIFFERENTIATION	2.34E-04	2.46E-02	4	BOC, CDON, IGFBP3, MEF2C
GO_OSTEOBLAST_DIFFERENTIATION	2.45E-04	2.55E-02	11	DLX5, ID4, IGFBP3, LEF1, MEF2C, PTH1R, SMAD6, SMOC1, SOX11, SPPI, TNC
GO_MUSCLE_ORGAN_MORPHOGENESIS	2.50E-04	2.57E-02	7	ANKRD1, COL11A1, COL3A1, HEY2, ISL1, MYL3, PROX1
GO_TELENCEPHALON_DEVELOPMENT	2.52E-04	2.57E-02	12	CDON, COL3A1, CXCL12, DLX2, DLX5, ID4, LEF1, LPAR1, PROX1, RELN, SLIT2, ZEB2
GO_CELL_CELL_SIGNALING	2.55E-04	2.58E-02	41	APCDD1, CDH11, CNTN4, CPE, CXCL14, DACT1, DLGAP1, DLX5, GABRP, GPC6, GRIN2A, GUCY1A1, HMG42, HRH2, ISL1, LEF1, LRRC4, LYPD1, MEF2C, NKD1, NOTUM, NTF3, OPRK1, PCDHB5, RASL10B, RBMS3, RELN, RGS4, SHISA6, SHISA9, SOSTDC1, SOX11, SPPI, SYTI0, TFAP2B, TNC, TNRC6C, TRHDE, WNT5B, ZEB2
GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DIFFERENTIATION	2.63E-04	2.63E-02	10	AUTS2, CDH11, DLX2, DLX5, ID4, ISL1, MAP2, PROX1, SLIT2, ZEB2
GO_UROGENITAL_SYSTEM_DEVELOPMENT	2.79E-04	2.75E-02	14	ACTA2, HAS2, ID4, IRX3, KCNJ8, KLHL3, MEF2C, PROX1, SLIT2, SMAD6, SOX11, SULF1, TFAP2B, TNC
GO_R_SMAD_BINDING	2.80E-04	2.75E-02	4	ANKRD1, RGCC, SMAD6, ZEB2
GO_SMOOTH_MUSCLE_CELL_MIGRATION	2.88E-04	2.79E-02	7	HAS2, IGFBP3, LPAR1, MEF2C, POSTN, SLIT2, SORL1
GO_SOMITE_DEVELOPMENT	3.29E-04	3.15E-02	7	CDX1, CDX2, CRB2, LEF1, NKD1, SOX11, ZEB2
GO_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	3.33E-04	3.15E-02	4	ADAMTS18, DMTN, PDPN, PRKCQ
GO_NEGATIVE_REGULATION_OF_NEURON_DIFFERENTIATION	3.35E-04	3.15E-02	11	CNTN4, DLX2, DPYSL3, ID4, IRX3, ISL1, LPAR1, MAP2, SEMA3D, SLIT2, SPPI
GO_FOREBRAIN_GENERATION_OF_NEURONS	3.38E-04	3.15E-02	6	AUTS2, DLX2, DLX5, LEF1, PROX1, SLIT2
GO_REGULATION_OF_AMPA_RECEPTOR_ACTIVITY	3.91E-04	3.62E-02	4	MEF2C, RELN, SHISA6, SHISA9
GO_CELL_PROLIFERATION_IN_BONE_MARROW	4.24E-04	3.80E-02	3	HMG42, LEF1, MEF2C
GO_FIBRILLAR_COLLAGEN_TRIMER	4.24E-04	3.80E-02	3	COL11A1, COL2A1, COL3A1
GO_SECRETORY_GRANULE_LOCALIZATION	4.24E-04	3.80E-02	3	KIF1A, MAP2, RASGRP1
GO_CARDIAC_MUSCLE_TISSUE_MORPHOGENESIS	4.30E-04	3.80E-02	6	ANKRD1, COL11A1, HEY2, ISL1, MYL3, PROX1
GO_POSITIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	4.30E-04	3.80E-02	6	AUTS2, CDON, COL3A1, LPAR1, RASGRP1, RELN
GO_DEVELOPMENTAL_CELL_GROWTH	4.36E-04	3.82E-02	11	AUTS2, CXCL12, MAPIB, MAP2, POSTN, RGS4, SEMA3D, SH3GL2, SLIT2, SPPI, ZEB2

GO_REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	4.65E-04	4.04E-02	6	GRIN2A, LYPD6B, ME2FC, RELN, SHISA6, SHISA9
GO_MUSCLE_STRUCTURE_DEVELOPMENT	4.72E-04	4.07E-02	21	ANKRD1, BOC, CDON, COL11A1, COL19A1, COL3A1, COL6A3, CTNNA2, CXCL14, HEY2, IGFBP3, ISL1, LEF1, ME2FC, MYL3, NKD1, PROX1, RGS4, SOSTDC1, SOX11, WFIKKN1
GO_REGULATION_OF_CELL_MORPHOGENESIS	4.76E-04	4.07E-02	17	CHN1, CXCL12, DMTN, FGD5, HAS2, LPAR1, MAP1B, MAP2, PDPN, POSTN, RELN, SDC2, SEMA3D, SLIT2, SPPI1, UST, ZEB2
GO_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_IN_CELL_CELL_SIGNALING	5.20E-04	4.39E-02	20	APCDD1, CPE, DACT1, DLX5, GPC6, GRIN2A, ISL1, LEF1, ME2FC, NKD1, NOTUM, RBMS3, RELN, RGS4, SHISA6, SOSTDC1, SULF1, TNRC6C, WNT5B, ZEB2
GO_RESPONSE_TO_ENDOGENOUS_STIMULUS	5.27E-04	4.39E-02	40	ADAMTSL2, AKR1C2, ANKRD1, CACNA1S, CDH13, COL2A1, COL3A1, CRB2, CXCL12, DLX5, DMTN, FLRT2, GDF6, GPR83, HAS2, HHIP, ISL1, LEF1, LPL, LYPD1, ME2FC, MXRA5, NR0B1, NREP, NTF3, OPRK1, PDE3B, POSTN, PRKCQ, SH3GL2, SLIT2, SMAD6, SOSTDC1, SOX11, SOX5, SPPI1, SULF1, TFAP2B, TNC, WFIKKN1
GO_MORPHOGENESIS_OF_AN_EPITHELIUM	5.27E-04	4.39E-02	18	DACT1, EDNRA, GPC6, HHIP, ID4, IRX3, KLHL3, LEF1, ME2FC, NKD1, PDPN, PROX1, SLIT2, SOSTDC1, SOX11, SULF1, TNC, ZEB2
GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PRODUCTION	5.31E-04	4.39E-02	4	C5, CYP1B1, ISL1, SULF1
GO_LENS_DEVELOPMENT_IN_CAMERA_TYPE_EYE	5.41E-04	4.43E-02	6	CDON, MAF, PROX1, SOX11, WNT5B, ZEB2
GO_HEART_DEVELOPMENT	5.45E-04	4.43E-02	19	ANKRD1, COL11A1, COL2A1, COL3A1, CPE, EDNRA, FLRT2, HAS2, HEY2, ISL1, KCNJ8, ME2FC, MYL3, PROX1, RGS4, SLIT2, SMAD6, SOX11, TENM4
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_STIMULUS	5.73E-04	4.62E-02	40	ADAMTSL8, ADAMTSL2, APCDD1, C5, COL2A1, COL3A1, CTNNA2, CXCL12, DACT1, DLX2, EYA2, HEY2, HHIP, HMG2, IGFBP3, ISL1, LPAR1, LPL, LRFN5, NKD1, NOTUM, NR0B1, PDE3B, PRKCQ, RBMS3, RGS4, RGS5, RNF152, SEMA3D, SH3GL2, SHISA6, SLIT2, SMAD6, SORL1, SOSTDC1, SPPI1, SULF1, UNC5B, WFIKKN1, WNT5B
GO_SOMITOGENESIS	5.83E-04	4.65E-02	6	CDX1, CDX2, CRB2, LEF1, NKD1, ZEB2
GO_CELLULAR_RESPONSE_TO_ENDOGENOUS_STIMULUS	5.86E-04	4.65E-02	35	ADAMTSL2, AKR1C2, ANKRD1, CACNA1S, COL2A1, COL3A1, CRB2, DLX5, DMTN, FLRT2, GDF6, HAS2, HHIP, ISL1, LEF1, LPL, LYPD1, ME2FC, NR0B1, NREP, NTF3, PDE3B, POSTN, PRKCQ, SH3GL2, SLIT2, SMAD6, SOSTDC1, SOX11, SOX5, SPPI1, SULF1, TFAP2B, TNC, WFIKKN1
GO_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	6.16E-04	4.85E-02	8	ACPP, GRIN2A, OPRK1, RELN, RGS4, SHISA6, SHISA9, TENM4
GO_EXTRACELLULAR_MATRIX_COMPONENT	6.25E-04	4.88E-02	5	COL11A1, COL15A1, COL2A1, COL3A1, TNC
GO_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	6.30E-04	4.88E-02	17	ANKRD1, CHN1, CTNNA2, CXCL12, DPYSL3, LPAR1, MAP1B, MAP2, ME2FC, NDNF, RELN, SDC2, SEMA3D, SLIT2, SPPI1, UST, ZEB2
GO_MUSCLE_CELL_MIGRATION	6.53E-04	5.02E-02	7	HAS2, IGFBP3, LPAR1, ME2FC, POSTN, SLIT2, SORL1
GO_HOMOPHILIC_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	6.62E-04	5.05E-02	9	CADM3, CDH11, CDH13, CDH7, CNTN4, PCDH18, PCDH7, PCDHB15, PCDHB5
GO_POSTSYNAPTIC_DENSITY_MEMBRANE	6.73E-04	5.06E-02	6	CNKS2, GRIN2A, LRFN5, LRRC4, SHISA6, SHISA9
GO_RESPONSE_TO_AXON_INJURY	6.73E-04	5.06E-02	6	DPYSL3, ISL1, MATN2, NREP, SPPI1, TNC
GO_POSITIVE_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	6.87E-04	5.12E-02	5	CRB2, ISL1, LEF1, PDPN, RGCC
GO_CARDIAC_SEPTUM_MORPHOGENESIS	7.22E-04	5.35E-02	6	HEY2, ISL1, PROX1, SLIT2, SMAD6, SOX11
GO_MUSCLE_TISSUE_DEVELOPMENT	7.43E-04	5.46E-02	15	ANKRD1, CDON, COL11A1, COL19A1, COL3A1, EYA2, HEY2, ISL1, LEF1, ME2FC, MYL3, PROX1, RGS4, SOX11, TENM4
GO_PALLIUM_DEVELOPMENT	7.84E-04	5.72E-02	9	CDON, COL3A1, DLX2, ID4, LEF1, PROX1, RELN, SLIT2, ZEB2
GO_REGULATION_OF_PLATELET_ACTIVATION	8.02E-04	5.81E-02	4	ADAMTSL8, DMTN, PDPN, PRKCQ
GO_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	8.23E-04	5.92E-02	8	CRB2, HAS2, HEY2, HMG2, ISL1, LEF1, PDPN, RGCC
GO_DNA_BINDING_TRANSCRIPTION_ACTIVATOR_ACTIVITY	8.61E-04	6.15E-02	15	CDX1, DLX2, DLX5, HMG2, HOXB5, HOXC4, ISL1, LEF1, MAF, MAFB, ME2FC, SOX11, TCF4, TFAP2B, ZEB2
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	8.85E-04	6.28E-02	12	ADAMTSL2, CRB2, HHIP, NREP, NTF3, SLIT2, SMAD6, SOSTDC1, SOX11, SULF1, TFAP2B, WFIKKN1
GO_COLLAGEN_FIBRIL_ORGANIZATION	8.98E-04	6.32E-02	5	ADAMTSL2, COL11A1, COL2A1, COL3A1, CYP1B1
GO_LENS_FIBER_CELL_DIFFERENTIATION	9.11E-04	6.35E-02	4	MAF, PROX1, WNT5B, ZEB2
GO_LIMBIC_SYSTEM_DEVELOPMENT	9.14E-04	6.35E-02	7	DLX2, ID4, LEF1, NR0B1, PROX1, RELN, ZEB2
GO_SMAD_BINDING	9.48E-04	6.53E-02	6	ANKRD1, COL3A1, HMG2, RGCC, SMAD6, ZEB2
GO_FOREBRAIN_NEURON_DIFFERENTIATION	9.79E-04	6.61E-02	5	AUTS2, DLX2, DLX5, PROX1, SLIT2
GO_INTRINSIC_COMPONENT_OF_POSTSYNAPTIC_DENSITY_MEMBRANE	9.79E-04	6.61E-02	5	GRIN2A, LRFN5, LRRC4, SHISA6, SHISA9
GO_VENTRICULAR_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	9.79E-04	6.61E-02	5	COL11A1, HEY2, ISL1, MYL3, PROX1
GO_HIPPOCAMPUS_DEVELOPMENT	1.01E-03	6.79E-02	6	DLX2, ID4, LEF1, PROX1, RELN, ZEB2
GO_RENAL_SYSTEM_DEVELOPMENT	1.03E-03	6.82E-02	12	ACTA2, HAS2, IRX3, KCNJ8, KLHL3, ME2FC, PROX1, SLIT2, SMAD6, SOX11, SULF1, TFAP2B
GO_REGULATION_OF_OLIGODENDROCYTE_DIFFERENTIATION	1.03E-03	6.82E-02	4	CXCR4, DLX2, ID4, TENM4
GO_INTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE	1.05E-03	6.91E-02	40	ABCC9, APCDD1, BOC, C5, CADM3, CD8B, CDON, EDNRA, FLRT2, GABRP, GPC6, GRIN2A, GRPR, GYPC, HAS2, HHIP, HRH2, KCNJ8, KCNMA1, LPAR1, LRFN5, LRRC4, OPRK1, PCDH18, PCDH7, PCDHB15, PCDHB5, PDPN, PTH1R, SEMA3D, SHISA6, SHISA9, SLC16A9, SLC24A3, SORL1, SYT13, TENM2, TENM4, TRHDE, TRPV6
GO_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA	1.06E-03	6.92E-02	11	ADAMTSL2, ANKRD1, COL3A1, ME2FC, MXRA5, NREP, POSTN, SMAD6, SOX11, SOX5, WFIKKN1
GO_METALLOPEPTIDASE_ACTIVITY	1.08E-03	7.02E-02	9	ADAM33, ADAMTSL8, ADAMTSL9, ADAMTSL2, CPE, CPQ, CPXMI, STAMBP1, TRHDE

GO_POSITIVE_REGULATION_OF_CHEMOKINE_SECRETION	1.12E-03	7.24E-02	3	C5, LPL, POSTN
GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PRODUCTION	1.16E-03	7.39E-02	4	C5, CYP1B1, ISL1, SULF1
GO_SUPRAMOLECULAR_FIBER_ORGANIZATION	1.17E-03	7.39E-02	20	ADAMTS2, ANKRD1, COL11A1, COL2A1, COL3A1, CTNNA2, CXCL12, CYP1B1, DMTN, DPYSL3, KIRRELI, LPAR1, MAP1B, MAP2, MEF2C, PHACTR1, PROX1, RGCC, RGS4, SLIT2
GO_REGULATION_OF_AXONOGENESIS	1.17E-03	7.39E-02	9	CHN1, CXCL12, MAP1B, MAP2, SEMA3D, SLIT2, SPP1, UST, ZEB2
GO_PDZ_DOMAIN_BINDING	1.22E-03	7.63E-02	6	LPAR1, NKD1, SDC2, SHISA6, SHISA9, SNTB1
GO_OSSIFICATION	1.23E-03	7.63E-02	14	CDH11, COL11A1, COL2A1, DLX5, ID4, IGFBP3, LEF1, MEF2C, PTH1R, SMAD6, SMOC1, SOX11, SPP1, TNC
GO_NEURAL_PRECURSOR_CELL_PROLIFERATION	1.24E-03	7.63E-02	8	CDON, HHIP, ID4, KIF1A, LEF1, PROX1, SOX5, ZEB2
GO_SEQUENCE_SPECIFIC_DNA_BINDING	1.24E-03	7.63E-02	29	CDX1, CDX2, DACH1, DLX2, DLX5, H2AFY2, HEY2, HMG42, HOXB5, HOXB6, HOXB8, HOXB9, HOXC4, HOXC8, IRX3, IRX6, ISL1, LEF1, MAF, MAFB, MEF2C, NR0B1, PRDM11, PROX1, SMAD6, SOX11, TCF4, TFAP2B, ZEB2
GO_AORTA_DEVELOPMENT	1.25E-03	7.64E-02	5	COL3A1, HEY2, PROX1, SMAD6, TFAP2B
GO_DEVELOPMENTAL_GROWTH	1.25E-03	7.64E-02	20	AUTS2, COL6A3, CPQ, CXCL12, HEY2, MAP1B, MAP2, MATN2, MEF2C, NKD1, POSTN, PROX1, RGS4, SEMA3D, SH3GL2, SLIT2, SPP1, TENM4, TNC, ZEB2
GO_HMG_BOX_DOMAIN_BINDING	1.37E-03	8.23E-02	3	DLX5, HOXC4, MEF2C
GO_PULMONARY_VALVE_MORPHOGENESIS	1.37E-03	8.23E-02	3	HEY2, SLIT2, SMAD6
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	1.40E-03	8.37E-02	13	ADAMTS2, COL3A1, CRB2, DLX5, GDF6, LEF1, NREP, SMAD6, SOSTDC1, SOX11, SULF1, TFAP2B, WFIKKN1
GO_AORTA_MORPHOGENESIS	1.45E-03	8.63E-02	4	COL3A1, HEY2, PROX1, TFAP2B
GO_NEURON_PROJECTION_REGENERATION	1.46E-03	8.65E-02	5	ISL1, MATN2, NREP, SPP1, TNC
GO_REGULATION_OF_BMP_SIGNALING_PATHWAY	1.56E-03	9.15E-02	6	CRB2, SMAD6, SOSTDC1, SOX11, SULF1, TFAP2B
GO_VENTRICULAR_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	1.64E-03	9.53E-02	3	HEY2, MEF2C, PROX1
GO_NEURAL_CRESCENT_CELL_DIFFERENTIATION	1.65E-03	9.53E-02	6	EDNRA, ISL1, MEF2C, SEMA3D, SOX11, ZEB2
GO_ROOF_OF_MOUTH_DEVELOPMENT	1.65E-03	9.53E-02	6	COL2A1, DLX5, LEF1, MEF2C, SOX11, WFIKKN1
GO_REGULATION_OF_GLUTAMATE_RECEPTOR_SIGNALING_PATHWAY	1.70E-03	9.76E-02	5	GRIN2A, MEF2C, RELN, SHISA6, SHISA9
GO_REGULATION_OF_WNT_SIGNALING_PATHWAY	1.71E-03	9.77E-02	13	APCDD1, DACT1, DLX5, ISL1, LEF1, NKD1, NOTUM, RBMS3, SHISA6, SOSTDC1, SULF1, WNT5B, ZEB2
GO_EPITHELIAL_TUBE_MORPHOGENESIS	1.79E-03	1.02E-01	12	EDNRA, HHIP, IRX3, KLHL3, LEF1, MEF2C, PROX1, SLIT2, SOSTDC1, SOX11, TNC, ZEB2
GO_OLIGODENDROCYTE_DIFFERENTIATION	1.85E-03	1.04E-01	6	CXCR4, DLX2, ID4, LPAR1, SOX11, TENM4
GO_REGENERATION	1.88E-03	1.06E-01	9	CPQ, CXCL12, ISL1, MATN2, NNMT, NREP, POSTN, SPP1, TNC
GO_REGULATION_OF_DNA_BINDING	1.93E-03	1.06E-01	7	HEY2, HMG42, ID4, ISL1, LEF1, SOX11, WFIKKN1
GO_AORTA_SMOOTH_MUSCLE_TISSUE_MORPHOGENESIS	1.94E-03	1.06E-01	2	COL3A1, PROX1
GO_POSITIVE_REGULATION_OF_PLATELET_ACTIVATION	1.94E-03	1.06E-01	2	DMTN, PDPN
GO_RESPONSE_TO_PROSTAGLANDIN_D	1.94E-03	1.06E-01	2	AKR1C2, TNC
GO_RESPIRATORY_SYSTEM_DEVELOPMENT	1.95E-03	1.06E-01	9	ADAMTS2, ADAMTS2L, DLX5, HHIP, LEF1, PDPN, PROX1, SOX11, TNC
GO_SENSORY_SYSTEM_DEVELOPMENT	1.98E-03	1.08E-01	13	ADAMTS18, CDON, CYP1B1, DLX2, ISL1, MAF, NKD1, PROX1, SMOC1, SOX11, TFAP2B, WNT5B, ZEB2
GO_BASEMENT_MEMBRANE	2.06E-03	1.12E-01	6	COL15A1, COL2A1, FREM1, MATN2, SMOC1, TNC
GO_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	2.08E-03	1.12E-01	10	ADAMTS2, CRB2, GDF6, NREP, SMAD6, SOSTDC1, SOX11, SULF1, TFAP2B, WFIKKN1
GO_CIRCULATORY_SYSTEM_PROCESS	2.15E-03	1.15E-01	17	ABCC9, ACTA2, ACNA1S, CELF2, CES1, CXCL12, EDNRA, GUCY1A1, HEY2, HRH2, KCNJ8, KCNMA1, MYL3, POSTN, RASL10B, RGS4, SLIT2
GO_MUSCLE_ORGAN_DEVELOPMENT	2.20E-03	1.17E-01	14	ANKRD1, CDON, COL11A1, COL19A1, COL3A1, COL6A3, HEY2, ISL1, LEF1, MEF2C, MYL3, PROX1, RGS4, SOX11
GO_POSTSYNAPTIC_MEMBRANE	2.21E-03	1.17E-01	12	CNKS2, CTNNA2, DLGAP1, GABRP, GRIN2A, KCNMA1, LRFN5, LRRC4, OPRK1, SHISA6, SHISA9, TENM2
GO_PROTEIN_HOMODIMERIZATION_ACTIVITY	2.25E-03	1.18E-01	23	ACPP, ADA2, APOBEC3G, CADM3, CDH11, CDH13, CDH7, CPQ, GDF6, HEY2, KIF1A, LPL, MAFB, NR0B1, PTH1R, RASGRP1, SH3GL2, SLIT2, SYT10, TCF4, TENM2, TENM4, TFAP2B
GO_NEURON_PROJECTION_EXTENSION	2.27E-03	1.18E-01	8	AUTS2, CXCL12, MAP1B, MAP2, POSTN, SEMA3D, SH3GL2, SLIT2
GO_CHEMOKINE_SECRETION	2.29E-03	1.18E-01	3	C5, LPL, POSTN
GO_COMPLEX_OF_COLLAGEN_TRIMERS	2.29E-03	1.18E-01	3	COL11A1, COL2A1, COL3A1
GO_PULMONARY_VALVE_DEVELOPMENT	2.29E-03	1.18E-01	3	HEY2, SLIT2, SMAD6
GO_POSITIVE_REGULATION_OF_SECRETION	2.35E-03	1.21E-01	14	AIM2, ANKRD1, C5, CXCL12, ISL1, LPL, OPRK1, POSTN, RASGRP1, RASL10B, RGCC, SOX11, SPP1, SYT10
GO_DOUBLE_STRANDED_DNA_BINDING	2.38E-03	1.21E-01	25	AFF3, AIM2, CDX1, CDX2, DACH1, DLX2, DLX5, H2AFY2, HEY2, HMG42, HOXB5, HOXB6, HOXB9, HOXC4, ISL1, LEF1, MAF, MAFB, MEF2C, PRDM11, PROX1, SMAD6, SOX11, TCF4, TFAP2B
GO_DOPAMINE_SECRETION	2.40E-03	1.21E-01	4	CXCL12, OPRK1, SYT10, SYT13
GO_REGULATION_OF_NEURON_MIGRATION	2.40E-03	1.21E-01	4	COL3A1, CTNNA2, FLRT2, RELN
GO_NEGATIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	2.42E-03	1.22E-01	6	DMTN, MAP2, POSTN, SEMA3D, SLIT2, SPP1
GO_NEGATIVE_REGULATION_OF_WNT_SIGNALING_PATHWAY	2.81E-03	1.38E-01	9	APCDD1, DACT1, ISL1, NKD1, NOTUM, RBMS3, SHISA6, SOSTDC1, WNT5B
GO_CELL_CELL_SIGNALING_BY_WNT	2.83E-03	1.38E-01	16	APCDD1, CPE, DACT1, DLX5, GPC6, ISL1, LEF1, NKD1, NOTUM, RBMS3, SHISA6, SOSTDC1, SULF1, TNRC6C, WNT5B, ZEB2

GO_SEQUENCE_SPECIFIC_DOUBLE_STRANDED_DNA_BINDING	2.84E-03	1.38E-01	23	CDX1, CDX2, DACH1, DLX2, DLX5, H2AFY2, HEY2, HMG2, HOXB5, HOXB6, HOXB9, HOXC4, ISL1, LEF1, MAF, MAFB, MEF2C, PRDM11, PROX1, SMAD6, SOX11, TCF4, TFAP2B
GO_POSTSYNAPSE	2.85E-03	1.38E-01	18	CNKS2, CTNNA2, DLGAP1, DMTN, GABRP, GRIN2A, KCNMA1, KIF1A, LPAR1, LRFN5, LRRC4, MAP1B, MAP2, MEF2C, OPRK1, SHISA6, SHISA9, TENM2
GO_CELL_CELL_ADHESION_MEDIATED_BY_CADHERIN	2.87E-03	1.38E-01	4	CDH11, CDH13, CDH7, RGCC
GO_NEGATIVE_CHEMOTAXIS	2.87E-03	1.38E-01	4	FLRT2, SEMA3D, SLIT2, UNC5C
GO_OLIGODENDROCYTE_DEVELOPMENT	2.87E-03	1.38E-01	4	ID4, LPAR1, SOX11, TENM4
GO_NETRIN_RECEPTOR_ACTIVITY	2.88E-03	1.38E-01	2	UNC5B, UNC5C
GO_POSITIVE_REGULATION_OF_DOPAMINE_SECRETION	2.88E-03	1.38E-01	2	CXCL12, OPRK1
GO_POSITIVE_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	2.88E-03	1.38E-01	2	DMTN, PDPN
GO_RNA_POLYMERASE_II_DISTAL_ENHANCER_SEQUENCE_SPECIFIC_DNA_BINDING	2.97E-03	1.42E-01	6	CDX1, CDX2, HOXB5, HOXB6, HOXC4, MEF2C
GO_POSTSYNAPTIC_SPECIALIZATION_MEMBRANE	3.13E-03	1.47E-01	6	CNKS2, GRIN2A, LRFN5, LRRC4, SHISA6, SHISA9
GO_REGULATION_OF_RESPONSE_TO_DRUG	3.13E-03	1.47E-01	6	CXCL12, HMG2, OPRK1, RGS4, SYT10, SYT13
GO_NEGATIVE_REGULATION_OF_PROTEIN_BINDING	3.28E-03	1.54E-01	6	DACT1, ISL1, LEF1, MAP2, SORL1, WFIKKN1
GO_BONE_DEVELOPMENT	3.30E-03	1.54E-01	9	CDX1, COL2A1, COL6A3, DLX5, FREM1, HAS2, MATN2, MEF2C, SULF1
GO_SYNAPTIC_MEMBRANE	3.31E-03	1.54E-01	14	CADM3, CNKS2, CPE, CTNNA2, DLGAP1, GABRP, GRIN2A, KCNMA1, LRFN5, LRRC4, OPRK1, SHISA6, SHISA9, TENM2
GO_CELL_GROWTH	3.33E-03	1.54E-01	15	AUTS2, CXCL12, IGFBP3, LEF1, MAP1B, MAP2, POSTN, PRDM11, PRKCQ, RGS4, SEMA3D, SH3GL2, SLIT2, SPPI, ZEB2
GO_REGULATION_OF_CHEMOTAXIS	3.40E-03	1.57E-01	9	C5, CDH13, CXCL12, CXCL14, CXCR4, LPAR1, NTF3, SEMA3D, SLIT2
GO_ENDOCHONDRAL_BONE_MORPHOGENESIS	3.53E-03	1.61E-01	5	COL2A1, COL6A3, DLX5, MATN2, MEF2C
GO_VENTRICULAR_SEPTUM_DEVELOPMENT	3.53E-03	1.61E-01	5	HEY2, PROX1, SLIT2, SMAD6, SOX11
GO_VENTRICULAR_SEPTUM_MORPHOGENESIS	3.70E-03	1.68E-01	4	HEY2, PROX1, SLIT2, SOX11
GO_GROWTH	3.71E-03	1.68E-01	25	AUTS2, COL6A3, CPQ, CXCL12, HEY2, HMG2, IGFBP3, LEF1, MAP1B, MAP2, MATN2, MEF2C, NKD1, POSTN, PRDM11, PRKCQ, PROX1, RGS4, SEMA3D, SH3GL2, SLIT2, SPPI, TENM4, TNC, ZEB2
GO_NEURON_TO_NEURON_SYNAPSE	3.77E-03	1.70E-01	12	CNKS2, CTNNA2, DLGAP1, DMTN, GRIN2A, LRFN5, LRRC4, MAP1B, MAP2, SH3GL2, SHISA6, SHISA9
GO_NEUROPEPTIDE_SIGNALING_PATHWAY	3.79E-03	1.70E-01	6	CPE, GPR83, GRPR, NXP2, OPRK1, TAC3
GO_POSITIVE_REGULATION_OF_LOCOMOTION	3.83E-03	1.71E-01	17	CDH13, CXCL12, CXCL14, DMTN, FAM110C, HAS2, LEF1, LPAR1, NTF3, OPRK1, PDPN, POSTN, PROX1, RELN, SEMA3D, SLIT2, WNT5B
GO_BLOOD_VESSEL_MORPHOGENESIS	3.97E-03	1.74E-01	19	C5, CDH13, COL15A1, COL3A1, CYP11B1, EDNRA, HAS2, HEY2, HMG2, ISL1, LEF1, NDNF, PDE3B, PROX1, RGCC, SLIT2, SULF1, TFAP2B, UNC5B
GO_ANTERIOR_POSTERIOR_AXON_GUIDANCE	3.99E-03	1.74E-01	2	UNC5B, UNC5C
GO_EMBRYONIC_RETINA_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	3.99E-03	1.74E-01	2	CDON, PROX1
GO_ENDOTHELIAL_CELL_FATE_COMMITMENT	3.99E-03	1.74E-01	2	PDPN, PROX1
GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_CHEMOTAXIS	3.99E-03	1.74E-01	2	LPAR1, SLIT2
GO_HETEROPHILIC_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	4.00E-03	1.74E-01	4	CADM3, CRB2, TENM2, TENM4
GO_REGULATION_OF_SUPRAMOLECULAR_FIBER_ORGANIZATION	4.32E-03	1.86E-01	12	CTNNA2, CXCL12, DMTN, KIRRELI, LPAR1, MAP1B, MAP2, MEF2C, PROX1, RGCC, RGS4, SLIT2
GO_CHONDROCYTE_DEVELOPMENT	4.33E-03	1.86E-01	4	COL11A1, COL6A3, MATN2, SULF1
GO_GLYCOSAMINOGLYCAN_BINDING	4.46E-03	1.91E-01	9	ADA2, COL11A1, DPYSL3, LPL, NDNF, POSTN, SERPINA5, SLIT2, SULF1
GO_CARDIAC_SEPTUM_DEVELOPMENT	4.55E-03	1.94E-01	6	HEY2, ISL1, PROX1, SLIT2, SMAD6, SOX11
GO_NEGATIVE_REGULATION_OF_SIGNALING	4.60E-03	1.96E-01	32	ADAMTSL2, APCDD1, COL2A1, CXCL12, DACT1, DLX2, EYA2, HEY2, HHIP, IGFBP3, ISL1, LPAR1, NKD1, NOTUM, NR0B1, OPRK1, PDE3B, PRKCQ, RBMS3, RGS4, RGS5, RNF152, SH3GL2, SHISA6, SLIT2, SMAD6, SORL1, SOSTDC1, SULF1, UNC5B, WFIKKN1, WNT5B
GO_CALCIIUM_DEPENDENT_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	4.67E-03	1.97E-01	4	CDH11, CDH13, CDH7, PCDHB5
GO_REGULATION_OF_LAMELLIPODIUM_ORGANIZATION	4.67E-03	1.97E-01	4	AUTS2, DMTN, PDPN, SLIT2
GO_INTRINSIC_COMPONENT_OF_POSTSYNAPTIC_SPECIALIZATION_MEMBRANE	4.70E-03	1.97E-01	5	GRIN2A, LRFN5, LRRC4, SHISA6, SHISA9
GO_NERVE_DEVELOPMENT	4.70E-03	1.97E-01	5	ISL1, LPAR1, MAFB, NTF3, SULF1
GO_NEGATIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_PROCESS	4.93E-03	2.05E-01	30	ADAMTSL2, CTNNA2, COL3A1, DLX2, DPYSL3, GUCY1A1, HEY2, HOXB8, ID4, IRX3, ISL1, KCNMA1, LEF1, LPAR1, MAFB, MAP2, MEF2C, OPRK1, PDE3B, RGCC, RGS4, SEMA3D, SLIT2, SMAD6, SORL1, SOSTDC1, SOX11, SPPI, SULF1, TRIB2
GO_EXCITATORY_SYNAPSE	5.03E-03	2.09E-01	4	CADM3, CTNNA2, LRRC4, SHISA6
GO_CALCIIUM_ION_BINDING	5.07E-03	2.10E-01	19	CDH11, CDH13, CDH7, CRB2, LPL, MATN2, MYL3, NKD1, PCDH18, PCDH7, PCDHB15, PCDHB5, RASGRP1, SLIT2, SMOC1, SULF1, SYT10, SYT13, TENM2
GO_CENTRAL_NERVOUS_SYSTEM_PROJECTION_NEURON_AXONOGENESIS	5.11E-03	2.10E-01	3	CDH11, SLIT2, ZEB2
GO_OUTFLOW_TRACT_MORPHOGENESIS	5.24E-03	2.13E-01	5	HEY2, ISL1, MEF2C, SMAD6, SOX11

GO_DENSE_CORE_GRANULE_TRANSPORT	5.27E-03	2.13E-01	2	KIF1A, MAP2
GO_EXCITATORY_CHEMICAL_SYNAPTIC_TRANSMISSION	5.27E-03	2.13E-01	2	GRIN2A, SHISA6
GO_LYMPHATIC_ENDOTHELIAL_CELL_DIFFERENTIATION	5.27E-03	2.13E-01	2	PDPN, PROX1
GO_POSITIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	5.35E-03	2.16E-01	7	CXCL12, DMTN, HAS2, MAP1B, RELN, SLIT2, ZEB2
GO_AXON_REGENERATION	5.41E-03	2.16E-01	4	ISL1, NREP, SPP1, TNC
GO_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	5.41E-03	2.16E-01	4	DMTN, HAS2, PDPN, POSTN
GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DEVELOPMENT	5.53E-03	2.19E-01	5	AUTS2, CDH11, MAP2, SLIT2, ZEB2
GO_ORGANELLE_TRANSPORT_ALONG_MICROTUBULE	5.53E-03	2.19E-01	5	DYNC1H1, KIF1A, MAP1B, MAP2, RASGRP1
GO_DNA_BINDING_TRANSCRIPTION_FACTOR_ACTIVITY	5.62E-03	2.22E-01	37	AFF3, CDX1, CDX2, CERS6, DACH1, DLX2, DLX5, HEY2, HMG2, HOXB5, HOXB6, HOXB8, HOXB9, HOXC4, HOXC8, ID4, IRX3, IRX6, ISL1, LEF1, MAF, MAFB, MEF2C, NR0B1, PRDM11, PROX1, RUNX1T1, SMAD6, SOX11, SOX5, TCF4, TFAP2B, ZEB2, ZNF439, ZNF521, ZNF618, ZNF660
GO_REGULATION_OF_POSITIVE_CHEMOTAXIS	5.72E-03	2.25E-01	3	CDH13, CXCL12, NTF3
GO_VESICLE_CYTOSKELETAL_TRAFFICKING	5.80E-03	2.28E-01	4	DYNC1H1, KIF1A, MAP2, RASGRP1
GO_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	5.92E-03	2.31E-01	9	ANKRD1, COL11A1, HEY2, ISL1, MEF2C, MYL3, PROX1, RGS4, TENM4
GO_DOPAMINE_TRANSPORT	6.22E-03	2.42E-01	4	CXCL12, OPRK1, SYT10, SYT13
GO_REGULATION_OF_SYSTEM_PROCESS	6.27E-03	2.43E-01	17	ABCC9, ACPP, CACNA1S, CELF2, GRIN2A, GUCY1A1, HEY2, HRH2, KCNMA1, MYL3, OPRK1, PDE9A, RELN, RGS4, SHISA6, SHISA9, TENM4
GO_QUATERNARY_AMMONIUM_GROUP_BINDING	6.36E-03	2.45E-01	3	PCYT1B, RASGRP1, SERPINA5
GO_REPLACEMENT_OSSIFICATION	6.36E-03	2.45E-01	3	COL2A1, DLX5, MEF2C
GO_AXON_EXTENSION	6.40E-03	2.45E-01	6	AUTS2, CXCL12, MAP1B, MAP2, SEMA3D, SLIT2
GO_REGULATION_OF_BINDING	6.51E-03	2.47E-01	12	CDON, DACT1, HEY2, HMG2, ID4, ISL1, LEF1, MAP2, MEF2C, SORL1, SOX11, WFIKK1
GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_BY_RNA_POLYMERASE_II	6.52E-03	2.47E-01	21	ANKRD1, CDX2, DACH1, DACT1, DLX2, H2AFY2, HEY2, HMG2, HOXB8, HOXC8, ID4, ISL1, LEF1, MAF, MEF2C, NR0B1, PROX1, SOX11, TENM2, TFAP2B, ZEB2
GO_STEM_CELL_PROLIFERATION	6.67E-03	2.47E-01	6	HHIP, HMG2, ID4, LEF1, SOX11, SOX5
GO_CEREBRAL_CORTEX_TANGENTIAL_MIGRATION	6.72E-03	2.47E-01	2	RELN, SLIT2
GO_EXTRINSIC_COMPONENT_OF_POSTSYNAPTIC_MEMBRANE	6.72E-03	2.47E-01	2	CNKS2, CTNNA2
GO_POSTSYNAPTIC_DENSITY_PROTEIN_95_CLUSTERING	6.72E-03	2.47E-01	2	LRRC4, RELN
GO_PURINE_NUCLEOBASE_METABOLIC_PROCESS	6.72E-03	2.47E-01	2	ACPP, URAD
GO_REGULATION_OF_SARCOMERE_ORGANIZATION	6.72E-03	2.47E-01	2	MEF2C, PROX1
GO_RELAXATION_OF_VASCULAR_SMOOTH_MUSCLE	6.72E-03	2.47E-01	2	GUCY1A1, KCNMA1
GO_SECONDARY_HEART_FIELD_SPECIFICATION	6.72E-03	2.47E-01	2	ISL1, MEF2C
GO_SMOOTH_MUSCLE_CELL_CHEMOTAXIS	6.72E-03	2.47E-01	2	LPAR1, SLIT2
GO_MORPHOGENESIS_OF_A_BRANCHING_STRUCTURE	6.90E-03	2.53E-01	8	DLX2, EDNRA, HHIP, LEF1, PROX1, SLIT2, SULF1, TNC
GO_DETECTION_OF_MECHANICAL_STIMULUS_INVOLVED_IN_SENSORIAL_PERCEPTION	7.05E-03	2.56E-01	3	COL11A1, CXCL12, PIEZO2
GO_PROSTATE_GLAND_MORPHOGENESIS	7.05E-03	2.56E-01	3	ID4, SULF1, TNC
GO_SYNAPSE_PART	7.12E-03	2.57E-01	23	CADM3, CNKS2, CPE, CTNNA2, DLGAP1, DMTN, GABRP, GRIN2A, KCNMA1, KIF1A, LPAR1, LRFN5, LRRC4, MAP1B, MAP2, MEF2C, NTF3, OPRK1, SH3GL2, SHISA6, SHISA9, SYT10, TENM2
GO_LAMELLIPODIUM_ORGANIZATION	7.13E-03	2.57E-01	5	AUTS2, CDH13, DMTN, PDPN, SLIT2
GO_GLIOGENESIS	7.23E-03	2.60E-01	10	APCDD1, CXCR4, DLX2, ID4, LEF1, LPAR1, MATN2, RELN, SOX11, TENM4
GO_RESPONSE_TO_WOUNDING	7.61E-03	2.73E-01	18	ADAMTS18, COL3A1, CPQ, DGKK, DMTN, DPYSL3, GRIN2A, ISL1, MATN2, NDNF, NREP, PDPN, POSTN, PRKCQ, SERPINA5, SPP1, TNC, WNT5B
GO_REGULATORY_REGION_NUCLEIC_ACID_BINDING	7.66E-03	2.73E-01	23	CDX1, CDX2, DACH1, DLX2, DLX5, H2AFY2, HEY2, HMG2, HOXB5, HOXB6, HOXB9, HOXC4, ISL1, LEF1, MAF, MAFB, MEF2C, PRDM11, PROX1, SMAD6, SOX11, TCF4, TFAP2B
GO_CARTILAGE_MORPHOGENESIS	7.79E-03	2.76E-01	3	COL6A3, MATN2, MEF2C
GO_CATENIN_COMPLEX	7.79E-03	2.76E-01	3	CDH11, CDH13, CDH7
GO_INTRINSIC_COMPONENT_OF_POSTSYNAPTIC_MEMBRANE	7.81E-03	2.76E-01	6	GRIN2A, LRFN5, LRRC4, OPRK1, SHISA6, SHISA9
GO_HEART_VALVE_DEVELOPMENT	8.08E-03	2.84E-01	4	HEY2, MEF2C, SLIT2, SMAD6
GO_AT_DNA_BINDING	8.32E-03	2.90E-01	2	HMG2, MEF2C
GO_CARDIAC_VENTRICLE_FORMATION	8.32E-03	2.90E-01	2	MEF2C, SOX11
GO_HINDBRAIN_RADIAL_GLIA_GUIDED_CELL_MIGRATION	8.32E-03	2.90E-01	2	CTNNA2, LEF1
GO_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	8.51E-03	2.95E-01	20	ADAMTS18, AIM2, APOBEC3G, C5, CDH13, CTNNA2, CXCL12, CXCL14, CXCR4, DMTN, ISL1, LPAR1, LPL, LRFN5, NTF3, PDPN, PRKCQ, SEMA3D, SLIT2, SPP1
GO_EXTRACELLULAR_MATRIX_BINDING	8.59E-03	2.97E-01	4	COL11A1, SLIT2, SMOG1, SPP1
GO_HEPARIN_BINDING	8.61E-03	2.97E-01	7	ADA2, COL11A1, LPL, NDNF, POSTN, SERPINA5, SLIT2

GO_REGULATION_OF_CELL_ADHESION	8.79E-03	3.02E-01	18	ADAMTS18, CDH13, COL26A1, CXCL12, CXCR4, CYP11B1, DMTN, HAS2, HLA-DPB1, LEF1, NDNF, PDE3B, PDPN, POSTN, PRKCQ, RASGRF1, RGCC, TNC
GO_REGULATION_OF_ACTIN_FILAMENT_BASED_PROCESS	8.97E-03	3.07E-01	12	CTNNA2, CXCL12, DMTN, KIRREL1, LPAR1, MEF2C, NTF3, PDPN, PROX1, RGCC, RGS4, SLIT2
GO_PLATELET_AGGREGATION	9.13E-03	3.11E-01	4	ADAMTS18, DMTN, PDPN, PRKCQ
GO_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	9.45E-03	3.21E-01	5	CRB2, ISL1, LEF1, PDPN, RGCC
GO_FILOPODIUM_ASSEMBLY	9.68E-03	3.26E-01	4	DMTN, DPYSL3, FGD5, TENM2
GO_NEUROBLAST_PROLIFERATION	9.68E-03	3.26E-01	4	HHIP, ID4, LEF1, SOX5
GO_EXOCYTIC_VESICLE	9.70E-03	3.26E-01	8	DPYSL3, GRIN2A, KIF1A, NTF3, OPRK1, SH3GL2, SYT10, SYT13
GO_ACTIN_FILAMENT_BASED_PROCESS	9.73E-03	3.26E-01	19	ANKRD1, AUTS2, CTNNA2, CXCL12, DMTN, DPYSL3, FGD5, KCNJ8, KIRREL1, LPAR1, MEF2C, MYL3, NTF3, PDPN, PHACTR1, PROX1, RGCC, RGS4, SLIT2
GO_INTRINSIC_COMPONENT_OF_SYNAPTIC_MEMBRANE	9.77E-03	3.26E-01	7	CADM3, GRIN2A, LRFN5, LRRC4, OPRK1, SHISA6, SHISA9
GO_GLIAL_CELL_DIFFERENTIATION	9.96E-03	3.26E-01	8	CXCR4, DLX2, ID4, LEF1, LPAR1, RELN, SOX11, TENM4

Supplemental Table S10. Gene ontology (GO) categories identified as associated (p-value<0.01) with genes expressed at significantly lower expression levels in hPSC-TS^{CDX2} vs. hPSC-TS cells. Gene ontology categories are listed along with their respective p-values of enrichment, false discovery rate (FDR)-adjusted p-values of enrichment, and specific genes relevant to each gene ontology category.

Gene Ontology Category	p-value	FDR-adjusted p-value	Number of Genes with Significantly Lower Expression in hTSCs vs. hTSCs within GO Category	Genes with Significantly Lower Expression in hTSCs vs. hTSCs within GO Category
GO_BONE_MINERALIZATION_INVOLVED_IN_BONE_MATURATION	8.33E-06	5.08E-02	4	LEP, LTF, PHOSPHO1, RFLNB
GO_BONE_MATURATION	1.02E-05	5.08E-02	5	LEP, LTF, PHOSPHO1, RFLNB, XYLT1
GO_ANIMAL_ORGAN_MATURATION	2.53E-05	8.44E-02	5	LEP, LTF, PHOSPHO1, RFLNB, XYLT1
GO_PEPTIDE_HORMONE_PROCESSING	1.03E-04	2.57E-01	5	BACE2, CGB3, LHB, PCSK1N, PCSK6
GO_CHONDROCYTE_DIFFERENTIATION	3.35E-04	6.70E-01	8	ACAN, COL6A1, ECM1, RFLNB, RUNX3, SHOX2, WNT10B, WNT7A
GO_CHONDROCYTE_DEVELOPMENT	5.64E-04	9.40E-01	5	ACAN, COL6A1, ECM1, RFLNB, SHOX2
GO_HORMONE_METABOLIC_PROCESS	1.40E-03	1.00E+00	10	ALDH1A1, BACE2, CGB3, HSD11B2, HSD3B1, LEP, LHB, PCSK1N, PCSK6, SLC5A5
GO_IODIDE_TRANSPORT	2.02E-03	1.00E+00	2	ANO1, SLC5A5
GO_N_FORMYL_PEPTIDE_RECEPTOR_ACTIVITY	2.02E-03	1.00E+00	2	GPR32, GPR32P1
GO_REGULATION_OF_BONE_MINERALIZATION_INVOLVED_IN_BONE_MATURATION	2.02E-03	1.00E+00	2	LTF, RFLNB
GO_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	2.46E-03	1.00E+00	5	HLA-F, HLA-G, LEP, UNC13D, VAV1
GO_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	2.54E-03	1.00E+00	12	ANO1, GABRE, MFSD2A, RTBDN, SLC12A3, SLC1A2, SLC22A11, SLC4A11, SLC52A1, SLC5A5, SLC6A8, SLC7A10
GO_NONASSOCIATIVE_LEARNING	3.00E-03	1.00E+00	2	MAPK8IP2, SHANK1
GO_CARTILAGE_DEVELOPMENT	3.22E-03	1.00E+00	9	ACAN, COL6A1, ECM1, LEP, RFLNB, RUNX3, SHOX2, WNT10B, WNT7A
GO_REGULATION_OF_BONE_MINERALIZATION	3.62E-03	1.00E+00	5	ECM1, LTF, PHOSPHO1, RFLNB, WNT10B
GO_BONE_DEVELOPMENT	3.77E-03	1.00E+00	9	COL6A1, FLI1, FOXC1, LEP, LTF, PHOSPHO1, RFLNB, SHOX2, XYLT1
GO_EXTRACELLULAR_MATRIX	4.09E-03	1.00E+00	16	ACAN, ANXA8, COL6A1, ECM1, FBLN2, LAMB3, LGALS1, MMP19, PCSK6, PHOSPHO1, RTBDN, S100A9, SLPI, SOD3, TFPI2, WNT7A
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I_VIA_ER_PATHWAY	4.15E-03	1.00E+00	2	HLA-F, HLA-G
GO_D_AMINO_ACID_TRANSPORT	4.15E-03	1.00E+00	2	SLC1A2, SLC7A10
GO_INTERMEDIATE_FILAMENT_BUNDLE_ASSEMBLY	4.15E-03	1.00E+00	2	KRT14, NEFM
GO_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	4.65E-03	1.00E+00	4	HLA-F, HLA-G, LEP, VAV1
GO_MULTI_MULTICELLULAR_ORGANISM_PROCESSES	5.08E-03	1.00E+00	9	HSD11B2, LEP, PSG1, PSG2, PSG3, PSG4, PSG5, PSG6, PSG9
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	5.40E-03	1.00E+00	4	BST2, HLA-F, HLA-G, JAK3
GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	5.41E-03	1.00E+00	3	BST2, HLA-F, JAK3
GO_BONE_MINERALIZATION	5.48E-03	1.00E+00	6	ECM1, LEP, LTF, PHOSPHO1, RFLNB, WNT10B
GO_NATURAL_KILLER_CELL_CYTOKINE_PRODUCTION	5.49E-03	1.00E+00	2	HLA-F, HLA-G
GO_NATURAL_KILLER_CELL_DEGRANULATION	5.49E-03	1.00E+00	2	HLA-F, UNC13D
GO_SEQUESTERING_OF_ZINC_ION	5.49E-03	1.00E+00	2	S100A9, SLC30A3
GO_CONNECTIVE_TISSUE_DEVELOPMENT	5.88E-03	1.00E+00	10	ACAN, COL6A1, ECM1, GPR4, LEP, RFLNB, RUNX3, SHOX2, WNT10B, WNT7A
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_EXOGENOUS_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_I_TAP_INDEPENDENT	6.99E-03	1.00E+00	2	HLA-F, HLA-G
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_PEPTIDE_ANTIGEN_VIA_MHC_CLASS_II	6.99E-03	1.00E+00	2	HLA-F, HLA-G
GO_MHC_CLASS_I_PROTEIN_COMPLEX	6.99E-03	1.00E+00	2	HLA-F, HLA-G
GO_N_ACETYLLACTOSAMINIDE_BETA_1_3_N_ACETYLGALACTOSAMINYLTRANSFERASE_ACTIVITY	6.99E-03	1.00E+00	2	B3GNT3, B3GNT7
GO_NEGATIVE_REGULATION_OF_TRANSCRIPTION_BY_COMPETITIVE_PROMOTER_BINDING	6.99E-03	1.00E+00	2	BHLHE41, HHX
GO_OVULATION_FROM_OVARIAN_FOLLICLE	6.99E-03	1.00E+00	2	LEP, MMP19
GO_KERATAN_SULFATE_BIOSYNTHETIC_PROCESSES	7.46E-03	1.00E+00	3	ACAN, B3GNT3, B3GNT7
GO_SKELETAL_SYSTEM_MORPHOGENESIS	7.90E-03	1.00E+00	9	ACAN, COL6A1, FOXC1, LTF, PHOSPHO1, RFLNB, SHOX2, WNT10B, WNT7A
GO_RESPONSE_TO_ZINC_ION	8.13E-03	1.00E+00	4	CKNK3, KRT14, MT4, SLC30A3
GO_LAMININ_BINDING	8.23E-03	1.00E+00	3	ECM1, LGALS1, LYPD5
GO_HORMONE_ACTIVITY	8.26E-03	1.00E+00	6	CGB1, CGB2, CGB3, CGB7, LEP, LHB
GO_NEGATIVE_REGULATION_OF_BONE_DEVELOPMENT	8.65E-03	1.00E+00	2	LTF, RFLNB

GO_POLY_N_ACETYLLACTOSAMINE_BIOSYNTHETIC_PROCESS	8.65E-03	1.00E+00	2	<i>B3GNT3, B3GNT7</i>
GO_REGULATION_OF_CHLORIDE_TRANSPORT	8.65E-03	1.00E+00	2	<i>ABCB1, GABRE</i>
GO_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	8.94E-03	1.00E+00	5	<i>ECM1, LTF, PHOSPHO1, RFLNB, WNT10B</i>
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	8.96E-03	1.00E+00	8	<i>BST2, HLA-F, HLA-G, JAK3, LEP, RAC2, UNC13D, VAV1</i>
GO_ANION_HOMEOSTASIS	9.21E-03	1.00E+00	4	<i>ABCG1, CA12, MLXIPL, SLC12A3</i>
GO_EXTRACELLULAR_MATRIX_BINDING	9.21E-03	1.00E+00	4	<i>ECM1, FBLN2, LGALS1, LYPD5</i>

Supplemental Table S11. Correlations between trophectoderm mRNA expression profiles (Petropolous et al.), and mRNA expression profiles from cell populations generated in the current study. Correlation R values are listed, as calculated based on the Spearman Rank correlation test correlating average expression levels per gene between datasets. All relationships were significant (p-value<0.0001).

Cell type	R value
hPSC-TS	0.7519
hPSC-TS ^{CDX2}	0.7562
placenta-derived TS	0.7594